

STIC Database Tracking Number: 1063

TO: Celine Qian

Location: CM1/11C01&11E12

Art Unit: 1636

Friday, October 24, 2003

Case Serial Number: 09/830703

From: Edward Hart

Location: Biotech-Chem Library

CM1-6B02

Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Qian,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: October 24, 2003, 07:28:57 ; Search time 7786 Seconds (without alignments) 17:68.751 Million cell updates/sec	Title: Perfect score: 3255 Seguence: 1 ctcagcgagggaaggggaaaaaaaaaaaaaaaaa 3255	Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0	Searched: 2885711 9eqs, 20454813386 residues	mber of hits sa	Mintmum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	10.00 10.00	

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PESSION AX089863 AX089863.1 GI:13443960 AX08085 Mus musculus (house mouse) PEGANISM Mus musculus Bukaryota; Metazoa; Chordata; Cramiata; Verrebrana; Euteleost Mammalia; Eutherna; Rodentia; Sciurognathi; Muridae; Murinae;	FINIT	Ä	2 0	ence	from	an or	3255 EP	۲.,٦	n i	-17 IW	<u>.</u>
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ORGANISM Mus musculus Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			M.s	r.osnw	lus (h	S O	onse				
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116: TITTTTCCCCCCRAMAGEN MACTOR CHATTOCHTTCCATTCCATTCCATTCCATCCATCCATCCATCCATC
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	RESULT 5 AX083882 LOCUS DEFINITION Sequence 20 from Patent Wollielre. AX083882 VRRSION AX083882 AX08382 AX083882 AX08382	Query Match 100.0%; Score 3233.4; DR 6; Length 3255; Best Local Similarity 100.0%; Pred. No. 0; Matches 3254; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	9y 1 CTCAGGGAGGGAAGGGAGGAGGAGGAGGAGAAACCTGACAAAACGTGGGG 60 1 CTCAGCGAGGAAGGGAGGAGGAGGAGGAGGGGG 60 1 CTCAGCGAGGAGGGAGGAGGAGCCTGGATGACTAAACCTGACAGAAAAACCTGGAGAAAGGGAGAGAGGAGAGAGA	9y 61 AGGCTCGGGGGGCCAGTGCCCGGGTAGGTCCTTCTGGACCGGCAGCCACCACCGCC 120	Qy 12: CGGTGACCATGATGTTGTCAGCTTCAACTCCAGCTATGGCTTCCCAGTGGAGGTCG 180 [
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REFERENCE 1 AUTHORS Luebbert, H. ITILE Transgenic animal model for neurodegenerative diseases JOURNAL Patent: EP 1091225-4 18 07-MAN-2001; Biofrontera Planmaceuticals AG (DE) FEATURES SOURCE 1.3256 A 1	Query Match	Oy 1 CTCAGGGGGGAAGGGGGGGGGGTGCTTAAACCTAAACGTGGAAAAGGTGGGG 60	Oy 61 AGGTCGGGCGGCGCGGTGCCGTAGGTCCTTCTCGACCCGCGCGCCGCC 120 [HTM] HTM] HTM] HTM] HTM] HTM] HTM] HTM]	Oy 121 CGGTGACCAFGATAGTGTTTGFCAGGTTCAACCTAGGTTCCCAGTGGAGGTCG 180 121 CGGTGACCAFGATGGTTTGFCAGGTTCAACTCCAGGTTTGFCAGTGGTTGAGGTTCGAGGTTGGTGAGGTTCAACTCCAAGTGGCTTCCCAGTGAAGGTGG 180	Oy 181 ATTCTGACACCAGCATOTTGCAGCACAGGAAGTGGTTGCTAAGCGACAGGGGGTTCCAG 240 [HT HT HT HT HT HT HT HT	2y 24J CTGACCAGCTSCATTTTTGCCGGGAAGGACTTCCGAATCACCTGACGGTTCAAA 300 24L CTGACCAGCTGCGTGTGATTTTTGCCGGGAAGGAGCTTCGGAATCACCTGACGGTTCAAA 300	OY 301 ACTGLOACTGGAACAACAGAGTATTGTACACATAGTACAGAGACCAGGAAGAGTC 360 1 1 1 1 1 1 1 1 1	Cy 361 ATGAAACAAATGCATCTGGAGGGACGAACCCCAGAGGCACCTCAGAGGGCTCCATATGG3 420		Oy 481 GSCTGGCGTCATTCTGGACACAGDAAGAGGATTCAGAAGCAGCCAGAGGTCCAG 540	Oy 541 TTAAACCCACCTACAACAGCTITTCATCTACTGCAAAGGCCCTGCCAAAGGTCCAGC 600	Oy 601 CTGGAAAGCTCCGAGTTCAGTGGCAACCAGCAAGCAACCCTCACCTTGGCCCAGG 660 1-11 11-11 11-111111111111111111111	661 GCCCATCTTGCTGGGACGATGTCTTAATTCCAAACCGGATGAGTGGAGTGCTGC 7 [5y 721 CAGACTGCCTGGAACCAGAGCTGAATTTTTTTTTTAATGTGGACCACACCTCGG 780 ill:ill11111111111111111111111111111111	Cy 781 ACAAGGACACGTCGGTAGCTTTGAACCTGATCACCAGCAGCAGCAGCAGCATCACTTGCA 843
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Mus musculus Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

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361 ATGAAACAAATSCATCTGGAGGGCCGAACCCCAGAGGGCTCCATATGGG 420 421 AGTCCAGGAGCTTGACACGAGGGCCTGAGCCGTGCGGGGGGGG	CTGGAAGCTCGAGTTCAGTGTGCGCCAACCAGCACCCCCCCC	181 ACANGRACIC GARACTITICAN CONTROL CANDER CONTROL BY A MANAGRACIA CANDER CONTROL BY A MANAGRACIA CONTROL BY A MANAGRACIA CANDER CONTROL BY A MANAGRACIA CONTROL BY A	CTGATT CAGTAT CA	GCT3CGGSTTGTTTCTGCCGGGACTGTAAGGAGGATACCATGAAGGGGATTGCGACT
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Query Match 100.0% Score 3253.4; DB 6; Length 3255;	CTGACACCAGGATTTTTGCCGGGAAGGACTTTTTGCCGGGAAGGACTTTTTTGCCGGGAAGGACTTTTTTTGCCGGGAAGGACTTTTTTTGCCGGGAAGGACTTTTTTTT	421 AGTCCAGGAGCTTGACACGAGTGGACCTGAGCGGCGTACCCTGCCGGTGGGCTCTGTGGG 421 AGTCCAGGAGCTTGACACGAGTGGACCTGAGCGGCTACCCTGCCGGTGGACTCTGTGG 421 AGTCCAGGAGCTTGACACGAGTGGACCTGAGCAGCCATACCCTGCCGGTGGACTCTGTGG 481 GGCTGGCGGTCATTCTGGACACAGACACGTTCAGAAGCAGCCAGAGGTCCAG 581 TTAAACCCACCTACAACAGCTTTTTCATCTACTGCAAAGGCCCTGCCAGAAGGTCCAGC 541 TTAAACCCACCTACAACAGCTTTTTCATCTACTAAAGGCCCTGCCACAAGGTCCAGC 541 TTAAACCCACCTACAACAGCTTTTTCATCTACTAAAGGCCCTGCCACAAGGTCCAGC 541 TTAAAACCCACCTACAACAGCTTTTTCATCTACTAAAAGCCCTGCCAAAAGGTCCAGC 541 TTAAAACCCACCTACAACAGCTTTTTCATCTACTACTAAAAGCCCTTGCCAAAAGGTCCAGC	601 CTGGAAAGCTCCGGGTTCAGTGTGGCACCTGCAAAGCAAGC	191 ACAAGGACACGTCGGTAGCTTTGAACCTGATCACCAGCAACAGCGCACCCTCCTTGC 191 ACAAGGACACGTCGGTAGCTTTGAACCTGATCACCAGCAACAGCGCACCACCCTTGC 191 ACAAGGACACGTCGGTAGCTTTGAACCTGATCACGACAACAGCGCAACAGCTCTTGC 191 ACAAGGACAGATGTCAGGAGCCCTGCCTGCTTTCCAGTGTAACCACCGTCACGTG 191 AGCGTGACAGATGTCAGGAGCCCTGTCCTGGTCTTCCAGTGTAACCACGTCACGTG 191 AGCGTGACAGATGTCAGTTGTATTGTCTCAAAGACTCAACGATCACGTCACGTG 191 ACGATGCTCAACTTGATTGTATTGTCAACAGATCAACGATCACGTG 191 ACGATGCTCAACTTGGTTTTGTGTCACAGAGCTCCCAACTTGTC 191 ACGATGCTCAACTTGGTTATTGTGTCACAGAGCTCCCAACTCCCTGATTTGTC 101 ACGATGCTCAACTTGGTTACCTCCCTGCCGTGTTGTCCAACACCCAACTCCCTGATTTGTC 102 AAGAGCTCCAACTTGGTACTCCCTGCCGTGTTGTGTCCAACTTCCCAACTCCCTGATTTGTC 102 AAGAGCTCCAACTTCACTTCACTCCCTGCCGTTGTTGTCCAACTTCCCTAACTTCTCTCAACATCCCCAACTCCCTGATTTTTTTT

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1681 TAGGGCACCCACAGAAACCACAGGCACCCCAGGGGGGGGG	1923 ATCHICTATECCRANGESCCCCTGCAGTAGTCAAAACTATTGTTTATCCCCCCAAAT 1980 1920 ATCATCTATCCCAAAGGGCCCCTGCAGTAGTCAAAACTATTGTTTATCCCCCCAAAT 1979 1920 ATCATCTTTACAAATGGTGCTGATGAGATTACAACCCCTGTGTACTAATCCCCCCAAAT 1979 1981 CCTATCTTTACAAATGGTGCTGATGAGATTACAACCCCTGTGTGTACTAATCAGGTTATC 2040 1982 CCTATCTTTACAAATGGTGCTGATGAGATTACAACCCCTGTGTGTATTAATCAGGTTATC 2039 2041 AACCAAGTGAGAAAGGTAAATTGGAGAGAGAGTGGTTAAATGGCAGGAGGA 2100 2040 AACCAAGTGAGAAAGCTAAATTGGATGGCAGACTGGTTAAATGGCAGGAGGA 2100 2040 AACCAAGTGAGAAAGCTAAATTGGATGGCAGACTGCTTAAATCGCAGGAGGA 2100 2040 AACCAAGTGAGAAAGCTAAATTGGATGGCAGACTGCTTAAATCGCAGGAGGA 2100	210: 210: 216: 216: 22: 222: 222:	2281 TTAAGAGACNATCCCATGATGCTGCGCCAATGCTAACAACAGGGTCAAGAACACATGT 23 2280 TTAAGAGACAATCCCATGATGCTGCGCCAATGCTAACAACAGGGTCAAGAACACAATGT 23 2281 TTATAGAAGAACATCCTGAACATGTGAATGAAGAGAACACTGAACAGT 23 2381 TTATAGAAGAACATCCTGAACATGTGAATGAAGAATATGCCTGACCCTTCCACGAACAAGA 24 2380 TTATAGAAGAAGCATCCCTGAACAATGAAGAAGATATGCCTGAACACATCCACGACACAACAAGAAGAACACATGCAATCCTCTGAATGAA	2461 CCACCCAGISGICCIACAGACAGGGAATACACACACCAAGAIAGCCIICAGAICAC 25 2460 CCACCCAGIGGICCIACACACACACACACACACAAGAIACAC 25 2521 AISCAICACACACAAACAGGGCAAIACACACACAACAAAACATATI 25 2521 AISCAICACACACAAGIGIAAICIIICAAGGIITTICIIIIICATIIICCIGIIIIIIII 25 2520 AIGCAICACACICAAGIGIIAAICIIICAAGGIITICIIIIICATIIICCIGIIIIIIII 25 2581 IGIIIICAGIIIIGCIIIITITIIITIIITITITITIAGGGGGCIACCAGTIIIIIII 25 2581 IGIIIIGCIIIIIGCIIIITITIIIITIIIITITIIIIGGGGGCIACCAACTIGAG 26	2580 IGHTHINITHINITHINITHINITHINITHINITHINITH
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Copyright (c) 1993 - 2003 Compuger Ltd.
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	AAFES260 standard; CDNA; 3255 BP. AAFES260; 29-XAY-2001 (first entry). Nucleotide sequence of a mutated murine parkin2 polypeptide. Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzhenzer: disease; Huntington's disease; amyotrophic lateral sclerosis; Multi-system atrophy, Milson's disease; pick's disease; Prion disease; brait tumour; head trama; stroke; vascular irregularity; metabolic irregularity; ss. Mus sp. Location/Qualifiers CDS //tag= a//frag= //frag= //	ouse parkin2 an animal as lish. TYP4558COP. TYP4558COP. TYP4558COP. TYP4558COP. TYP4558COP. TYP658COP. TYP6
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and secondary causes inducing Parkinson's syndromes like tox
brain tumours, head trauma, stroke, vascular irregularities
irregularities, associated with a less active or non-active
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                                  C; 808 G; 776 T; 0 other;
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The present sequence encodes a murine parkin2 polypeptide. The present sequence contains mutations, causing Asm54 to be changed to a stop odon, leading to a truncated protein. Wurations or deletions in the parkin2 parkinson of disease in humans. The numan parkin2 good of sease seed to a stop of the parkin2 good of sease. They are useful for analysing the rededeperative diseases. They are also useful for testing the floady of the treatment of a newrodedemerative disease such as parkinson's disease, Alzheimer's disease, Huntington's disease. The parkinson's disease, and sciences, muti-system atrophy, Misor's disease, pick's disease, pick indicates, and is encodeded training parkinson's syndromes like toxins, drugs, briain tumours, head training stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin protein.
                                                                                                                                                                                                                                                                                                                     Parkin2, Parkinson's disease, 6q25.2-27, neurodegenerative disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral solerosis, Multi-system atrophy, Wilson's disease, Pick's disease: Prion disease, brain tumour, head trauma; stroke, vascular irregularity,
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                                                     sequence of murine parking with a frameshift mutation.
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Parkin2: Parkinson's disease, 6925.2-27; neurodegenerative disease, Adateimer's disease, Huntington's disease, amyotrophic lateral sclerosis; Mulli-system atrophy, Wilson's disease, Pick's disease, Prich Gisease, brain tumour, head trauma; stroke; vascular irregularity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a murine parking polypeptibe. The polynucleotide sequence contains mutations, causing 31m38 to be changed to a top codon, leading to a truncated protein. Mutations or meletions in the parking gene Parkinson's disease in humans. The human parking gene is located in gene region 6q25.2-27, parking polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for insting the efficacy of the treatment of a neurodegenerative disease such as parkingon's disease, Alzbeiden's disease. Huntington's disease and polynucleotis, Multi-system atrophy, milson's disease, pion disease, Multi-system atrophy, milson's disease, prion disease, Multi-system atrophy, milson's disease, parkingon's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated
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                                                                                                                                                                                                                                                                                                                                                                                                                 of murine parkin2 with a frameshift mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding mouse parking protein, useful for
producing a transgenic non-human animal as an animal model for
neurodegenerative diseases
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                                                                                   TTTTTCCCCCTGAAAAGATAACAAAGTCTGCAAATTTGGTTTGGAGTATTCCTACTGCA
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The present sequence encodes a murine parking polypeptide. The polymcieotide Sequence contains mutations, causing Arg78 to be changed to a stop codon, leading to a truncated protesh. Whitations or deletions in the parking gene cause Parkinson's disease in humans or human parking gene is located in gene region 695.2-27 Parking polymcieotides and protection for analysing considerative disease. The parkinson of 695.2-37 Parking the parkinson of the treatment of a neurodegenerative disease. Price of a neurodegenerative disease such as a protection disease, hithmen's disease, hithmen's disease, hithmen's disease, hithmen's disease, and secondary causes inducing parkingon's syndromes like toxins, dangs, brain tumours, head graums, shock, wascular irregularities or retebolic inrequiarities, associated with a less active or non-active parkin prontin.
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                                                                                                                                                                                      Nucleotide sequence of murine parkin2 with a frameshift mutation
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producing a transgenic non-human animal as an animal model
meurodegenerative diseasos
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                                                   AAF55256 standard; cDNA; 3253 BP.
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Matches 3253; Conservative
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                                                                                                                       Parkin2, Parkinson's disease, 6q25.2-27, neurodegenerative disease, Alzhelmer's disease, Huntington's disease, amyorrophic lateral sclerosis, Multi-system atrophy, Wilson's disease, Plok's disease, Prion disease, brain turour, head trauma, stroke, vascular irregularity,
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Best Local Similarity 97.4%; Pred. No. C.
Matches 3170; Conservative C. Mismatches O. Indels 35;
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an animal model
                                                                          parkin2 with a frameshift
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129..713
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                                                                          Mucleotide sequence of murine
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                                                                        TTATAGAAGGAGCATCCCTCGACCATCTGAATGAGAGTATGCCTGACCCCTTCCACCACA
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The present sequence encodes a murine parking polypeptide. The polypucleotide sequence contains a frameshift mutation, leading to a trundaced protein, mutations or deletions in the parking gene cause Parkinson's disease in humans. The human parking gene is located in gene region 6q25.2-27. Parking polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alizheimer's disease, Huntington's disease, anyotrophic lateral sclerosis, Nulti-system atrophy, Milson's disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, bruin tumours, head traima stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin protein.
Multi-system atrophy, Milson's disease, Pick's disease, Prion disease, 
brain turour, head trauma, stroke, vascular trregularity:
metabolic irregularity; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   lectides encoding mouse parking profess, useful transgenic non-human animal as an animal model
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                                                                                                Location/Qualifiers
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Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis;
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The present sequence encodes a murine parking polypoptide. The polymordectide sequence contains a frameshift mutation, leading to a truncated protein. Mutations or deletions in the parkin2 gene cause parkinson's disease in humans. The human parkin2 gene is located in gene ragion 6452.2-27. Parkin2 polypetides and polymordectides takes are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Albrianer's disease, Huntingson's disease, anyotophic lateral sclerosis, Nulli-system arcophy, Mison's disease, prion disease, und secondary causes inducing trainal parkinson's syndromes like toxins, drugs, brain tumours, head trainal, strike, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCCCATCTTGCTSGGACGATGTCTAATTCCAAACCSGATGAGTSGTGAGTGCTGCTGTTTTCTTCAAACCGGATGAGTGCTGGTGAGTGTTTTCTGAACCGGATGAGTGGTGAGTGGTGAGTGTTAATTCCAAACGGGATGAGTGGTGGAGTGCGASTGT
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                                                                                                                                                                                                                          polynucleotides encoding mouse parkin2 protein, useful
Mucing a transgenic non-human animal as an animal model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3092 BP; 818 A; 778 C; 761 G; 735 T; 0 other;
           /*tag= a
/product= "truncated parkin2"
                                                                                                                                                                                                                                                                         Claim 3; Page 34-35; 62pp; English.
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                                                                                                                                                                                                                                                  neurodegenerative diseases
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                         ATGCATCACACTCAAGTGTTAATCTTTCAAGGTTTTTCTTTTCTTTTTCCTGTTTTTTATT
                                                       GAAAAGACCACCTGTCAAGCAGCAGTCAGAGTCTGATGTCACCCATCACTATTTTTT
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2717 GCCASSACAATGTTTGCTGTTTGGGTAAAGGGACTCCCTGAAGCTCTGTGGCTC 2776 2840 TCCAGTATGCTCCTTTTCCTTCTAACAGATGCATATTTTTTCAGAATACAATAGT 2899 2777 TCCAGTATGGTCCTTTTCCTTCCTAACAGATGCATATTTTTTTCAGAATACAATAGT 2836 29 0 GATTTTAAATAAATAGAAGAGAGAGAATGCATGTGTGAGCATGAATACATAGT 2836 2837 GATTCTTAAAATAAAATAGAAGAGAGAGATGCAAGAATACAATAGT 2896 2837 GATTCTTTAAAATAAAAAAAGAGAAAAAGAGAGAGAATCAAACCT 3119 2897 CATTGTGTGAAAAAAAAAAAAAAAGAGAATGAAAAAAAAA	111 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3077 AAAAAAAAAAAAA 3092 SULT 11	AAF55253; AAF55253; 29-WAY-2001 (first entry)	Ch. Nucleotide sequence of murine parkin2 with a frameshift mutation. XX XX XX XX XX XX XX XX Alzheimer's disease; 6q25.2-27; neurodegenerative disease; XX Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; XX Multi-system arrophy; Wilson's disease; Pick's disease; Prion disease; XX Mutative had trauma; stroke; vascular irrequiarity; XX Mutative disease; XX Mut			C7-WAR-2001.	PF 3C-AUG-1999; 99EP-Cli6766. XX PR 30-AUG-1999; 99EP-Cl16766.	AX (BIOF-) BIOFRONTERA PHARM GMBH. XX PI Luebbert H;		PT New polynucleotides encoding mouse parkin2 protein, useful for PT producing a transgenic non-human animal as an animal model for PT neurodegenerative diseases . *x	PS Claim 3; Page 29-30; 62pp; English. XX CC The present sequence encodes a murine parkin2 polypeptide. The CC Polynucleotide sequence contains a frameshift mutation, leading to a

1921 ATCATCTATTCCCAAAGGGCCCCTGCAGTAGTCAAAACTATTGTTTATCCCCCCAAAT 1980	1981 CCTATCTTTACAAATGGTGGTGATGACATTACAACCCTGTGTACTAATCAGGTTATC 2040	2041. NACCHAGTSAGANACTAGGAAGTGATTGGATGGCAGAGTTGAATCGCGGGGAGGA 2100 [HELLITTEL HELLT HELT HE	2131 ODGAGAAGCCAAACCTACGTTGGTTGATTATGGGGAACTTAGAAAAAATGTG 2163 	216; ITTITICCCCCTGAAAAGATAACAAAGCTSCAAITIGGITIGGAGTAITCCTACTGCA 2220 	222. gectggaagittagetteatgigaattiaacagaaaaagiseetataaaogggscott 2232 2200 sectggaagittagettoagtstaaattiaacagacaaasisetataaagggscotti 2668		234: TTATAGAGGASCATCCCTSGACCATCTGAATGASGGATGCCTGACCCCTTCSACGACA 2400 2:29 TTATAGAAGGACCTCGGACCATCTGAATGASAGTATSCTGACCCCTTCCACCACA 2188	2401 AGTGGGGACGCCTCTGCATATCTGCTCCTCCTCGTGTTAAGCCCCAGGGAGCCCAT 2460 (111. [11. [111. [111. [111. [111. [111. [111. [111. [111. [111. [111. [11. [11. [111. [111. [111. [111. [111. [111. [111. [111. [111. [111. [11. [11. [111. [111. [111. [111. [111. [111. [111. [111. [111. [111. [11. [11. [11. [111. [111. [111. [111. [111. [111. [111. [111. [11. [111. [111. [111. [111. [111. [111. [111. [111. [111. [111. [11. [111. [1. [2461 CCACCCAGIGGICCTACAGACAGGCAAIACACACACACAGAIAGCCTTGAGAICAAG 2520 [A AGGATCACACTGAAGGTTAATCTTTGAAGGTTTCTTTTCTTTTTCTGTTTTTATT 	2581 TOTTITICCTITICCTITITITITITITITITITICGROGGGGGGCTACCAACTIGAS 2640 [1, 111, 11]	occtagagctaaaaatcatatagaaatgatgttattgtggtgtgaggaaggccagct 			2921 CCATCATTGISCTISCCICTSCCICCTTCCACACCCGTSISACGTAATCSCAITGGGAAS 2880 [1,1] [2891 CCAGGACAATGTTTGCTGTTTGGGTAAAGGGACTCCCTGAAGCTCTGTGGCTCT 2943 [2841 CCAGIATGGTCCCTTTTCCTTCCTAACAGATSCATATGTTTCTTCASAATACAATAGTG 3000
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Pick's disease, Prion disease, and secondary causes inducing
Parkinson's syndromes like toxins, drugs, brain tumcurs, head trauma,
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Multi-system arrophy, Wilson's disease; Pick's disease; Prion disease;
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                                                                                                                                                                                                      The present sequence encodes a murine parkin2 polypeptide. The present sequence contains a frameshift mutation, leading to a truncated protein. Mutations or deletions in the parkin2 gene cause Parkinsch's disease in humans. The human parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for analysing meurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as parkinson's disease, Alzhaimer's disease, Hunington's disease, amyotrophic lateral sclerosis, Multi-system atrophy, Milson's disease, Pick's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated
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                                                                               New polynucleotides encoding mouse parkin2 protein, useful
producing a transgenic non-human animal as an animal model
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Alzheimer's disease; Huntington's disease; anyotrophic lateral solerosis;
Multi-system atrophy; Milson's disease; Pick's disease; Prion disease;
Erani timour; head trauma; Stroke; vascular irregularity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes a murine parkin2 polypeptide. The polymorleotide sequence contains a frameshiff mutation, leading to a truncated protein. Mutations or deletions in the parkin2 gene cause parkinson's disease in humans or the human parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polymorleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as parkinson's disease, Alzhehimer's disease, Huntingtor's disease, pick's disease, Prion disease, and secondary causes inducing parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAACCATCAAGAAGACCACCAAGCTTGTCCTCGCTGCAACGTGCCAATTGAAAAAACS
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Pred. No. 0;
0; Mismatches
                     62pp; English
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Best Local Similarity 99.9%;
Matches 2262; Conservative
                     Claim 3; Page 24-25;
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51 ACACCCGTGTGACGTAATCGCATTGGGAAGCCAGGACAATGTTTGCTGTTCTGCTTTTGG 2910	11 TAAAGGACTCCCTGAAGCTCTGTGGCTCTCCAGTATGGTCCCTTTTTCCTTCC	71 TGGATATGITTTCTCAGAATAGAATAGATCTTAAAATAACCGAAAGAGAGGGATC 3036 	3. CACAGIGIGAGCATGAATCACAGCCTGCATGIGIGAGIGIGAATAGIGGGATAAAG 3030 	9: TGGATGTGAGAGAGTGGAAATGAAACTCTGGAAAGGAATCTTTCTCTTTCTGTGAAGT 3150 	51 GTATTAAGAATACCTSAAGTCTGTGTGTGTGGTACCCAGACTGTCAATCAATAAAG 5210 	11 ACCCAGACTGTCAATGAAAAAAAAAAAAAAAAAAAAAAA
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Search completed: October 24, 2003, 10:10:13 Job time: 596 secs

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29. App. 29. App. 29. App. 29. App. 29. App. 17. App. 17. App. 22. App. 17. App. 17. App. 17. App. 17. App. 27. App. 27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/09680420A
Patent No. 622826
GENERAL INPORMATION:
APPLICANT: GILAD, Shlomit
APPLICANT: GILAD, Shlomit
APPLICANT: GROSNAN, Avita;
TILE OF INVENTION: MINDE POR ENRICHMENT OF NATURAL ANTIGENSE MESSENGER FILE PREFERENCE: GILADE A
CURRENT APPLICATION NUMBER: US/09/680,420A
CURRENT APPLICATION NUMBER: 60/157,843
FRIOR PILING DATE: 1999-10-66
NUMBER OF SEQ IN MOSE: 60/157,843
FRIOR FILING DATE: 1999-10-66
NUMBER OF SEQ IN MOSE: 60/157,843
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                    US-09-112-5620-25
US-09-172-42A-13
US-09-172-42A-13
US-08-263-473-17
US-08-263-473-17
US-09-264-615-59
US-09-264-615-59
US-09-152-060-22
US-09-152-060-22
US-09-152-060-22
US-09-152-060-22
US-09-152-060-22
US-09-244-48-12
US-09-24-448-12
US-09-24-448-12
US-09-24-448-12
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US-39-328-965-1/c
, Sequence 1, Application US/09328965
, Patent No. 6501008
, GENERAL INFORMATION:
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SEQ ID NO 26
LENGTH: 563
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ONGANISM: Artificial Sequence
FEATURE:
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Marches 127: Conservative
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
                            GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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US-08-09-1725-24
US-08-801-725-24
US-08-801-725-24
US-09-340-154-93
US-09-482-93
US-08-18-93
US-08-18-92
US-08-18-92
US-08-18-92
US-09-346-154-92
US-09-346-154-92
US-09-346-158-92
US-09-346-158-92
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US-09-18-92
US-09-216-27-1
US-09-516-27-1
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US-09-36-277-3
US-08-462-092-1
US-08-46-922-1
US-09-094-350-1
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Perfect score:
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Maximum DB
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                                        3403 recreachachicchonnadhaichacachthachthaidearchachtachagada 3468
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        236 TOCKBOTGACGAGCTGTGTGATTTTTGCCGGGAAGSAGCTTCCGAATGACCTGAGGGT 295
                                                                                                            296 TCNAMACTGTGACCTGGNACAACAGAGTATTGTACACATAGTACAGAACCACGAGGAG 355
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                                                                                                                                                                                                                                                                                                                                                                                                                  Paten,

OBMERAL INFORM.

APPLICANT: Peter H. Christens.

APPLICANT: Alan E. Christens.

APPLICANT: Howard P. Hershey

APPLICANT: Howard P. Hershey

APPLICANT: Thomas D. Sullivan

TILES F. INVENTION: PLANT UBIQUITIN PROMOTER SYSTEM

NUMBER OF SECTENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: ALAI Lloyd

SPEET: SLIE Lloyd

STREET: SLIE Lloyd

CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCRREAL MASSIAND CATALOGY ASSISTANCE OF CONTRACT Release #1.0, Version #1.25 CCRREAT APPLICATION CATA. PROPERTY NUMBER: US/08/462.052 FILING DATE: 5-JUNE-1995 CLASSIFICATION: 435 JUNE-1995 ATTORNEY/AGRIT INFORMATION: NAKE: 10943 J&6 FRETRICATION NUMBER: 35,569 REFERENCE/DOCKET NUMBER: 36,462,032 FELECOMMINICATION INFORMATION: TELEFONE: 904,375,8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    JS-08-462-092-1
| Sequence 1, Application US/08462092
| Patent No. 5614399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLGGY: linear MCLECULE TYPE: DNA (genomic) MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO. 1:
SEQUENCE GRARACTERISTICS:
LENGTH: 3840 base pairs
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904-372-5800
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                                                                                                                                                                                                                                                                     3469 CATGCA 3474
                                                                                                                                                                                                                 356 AAGTCA 361
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 ccgccccgrdaccargaragrarrgrcacgrrcaacrccaccrargecrrccagraga 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3229 CCTCCGTGGTGGCATGTTTGTCAAGACACTGACGGCAAGACCATCACCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: maize coleoptile endo-1,3;1,4-beta glucanase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.8%; Score 59.4; DB 4; Length 1091; Best Local Similarity 65.4%; Pred. No. 1.4e-06; Attches 87; Conservative 9; Mismatches 46; Indels C
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Best Local Similarity 52.4%; Pred. No. 5.2e-06;
Matches 129; Conservative 0; Mismatches 117; Indels
APPLICANT: Nevins, Donaid J.
APPLICANT: Simmons, Carl
APPLICANT: Simmons, Carl
APPLICANT: The Regents of the University of California
TITLE TO INVENTION: Endo. and Exo-Glucanases and Gene
FILE REPERENCE: 023070-096600US
CURRENT APPLICATION NUMBER: US(09/128,965
CURRENT FILING DATE: 1999-06-09
EARLIER APPLICATION NUMBER: US 60/088,780
EARLIER PILING DATE: 1998-36-10
NUMBER OF SEQ 10 NOS: 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/C9516277

Baten No. 6528701

CENERAL INCENTATION:
APPLICANT: WANG -- OARD
TITLE OF INVENTION: RICE UBLCUITIN-DERIVED PROMOTERS
FILE REFERENCE: 98AS
CURRENT FILING DATE: 200-02-29
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . LOCATION: (68)..(979)
: OTHER INPORMATION: endo-1,3/1,4-beta glucanase
US-39-328-965-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) NAME/KEY: CDS
; LOCATION: (2786)..(4159)
US-09-516-277-3
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CRGANISM: Cryza sativa
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LOCATION: (68
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US-09-516-277-3
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2616 TSCCGACTACAACATCCAGAAGAGAGACCCTCCACTTGGTGCTGCGCCTCAGGGAGG 2675
                                                                                                             2556 TCCCCCAGACCAGCAGCAGCTCTTTGCTGGAAAGCAGCTTGAGGACGGGCGCACGCT
                                                                                                                                                          296 TCAAAACTGTGACCTGGAACAACAGAGTATTGTACACATAGTACAGAGACCACGOAGGAG
                                                                  236 TCCAGCTGACCAGCTGCGTGTGATTTTTGCCGGGAAGGAGCTTCCGAATCACCTGACGGG
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52.0%; Pred. No. 1.3e 05/
tive 0: Mismatches 118/ Indexs D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Peter H. Quail
APPLICANT: Peter H. Christensen
APPLICANT: Alar H. Christensen
APPLICANT: Howard P. Hershey
APPLICANT: Howard D. Sulivan
TITLE DF INVENTION: P.ANT UBIQUITIN PROMOTER SYSTEM
NUMBER OF SEQUENCES: 2
ADDRESSYDENCES: 2
ADDRESSYDENCE ALORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCUNTRY: USA

ZIP: 32606
COMPUTER SEADABLE FCRN:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.3, Vorsion #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8: Jeff Lloyd
2421 N.W. 41st Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08/462,092
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FILING DATE: 5.0NE.1995
ATTORNEY-AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35.589
REFRENCE/DOCKET NUMBER: 08/4/
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                       Segmence 1, Application US/09094350
Patent No. 6054574
GEWERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
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SEQUENCE CHARACTERISTICS:
LENGTH: 3840 base pair
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1993..3591
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nuclesc acid
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Best Local Similarity
Matches 128; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
US-09-094-350-1
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US-09-094-350-1
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                              2556 TCCCCCAGACCAGCAGCGCTCATCTTTGCTGGAAAGCAGCTTGAGGACGGCGCACGCT 2615
                                                                                                                                  2616 TGCCGACTACAACATCCAGAAGGAGCACCCTCCACTTGGTGCTGCGCCTCAGGGGAGG 2675
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236 TCCAGCTGACCAGCTGCGTGATTTTTGCCGGGAAGGAGCTTCCGAATCACCTGACGGT 295
                                                                                     TCAAAACTGTGACCTGGAACAACAGGTATTGTACACATAGTACAGAGACCACGGAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPALIBLE
COBERATING SYSTEM: PC-DOS/MS-DCS
SOFTWARE: RatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,822
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Alan H. Christensen
APPLICANT: Alan H. Christensen
APPLICANT: Robert A. Sharrock
APPLICANT: Robert A. Sharrock
TITLE OF INVENTION: PLANT UBLIQUITIN PROMOTER SYSTEM
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jeff Lloyd
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: JS/08/462,092
FILING DATE: S-JUNE-1935
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
RGGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: 28/462,092
REFERENCE/DOCKET NUMBER: 08/462,092
TELEPAN: 904-275-910
INFORMATION FOR SEQ 10 NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1949 DASE PAIRS
                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08746822
Patent No. 6020190
GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
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LCCATION: 1993..3591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Gai
STATE: FI
COUNTRY:
                                                                                                                                                                                                                                                                                                               US-08-746-822-1
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GENERAL INFORMATION
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                                                                                                                      ADDRESSEE:
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Marches 142;
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ORIGINAL SO
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                                 2436 CCTCAGGGGAGGCATGCAGATCTTCGTGAAGACCTGACCGGCAAGACTATCACCCTCGA 2495
                                                                                                         2496 GGTGGAGTCTTCAGACACCATCGACAACGTCAAGGCCAAGATCCAGGACAAGGAGGGCAT 2555
                                                                                                                                                            295
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116 CCGCCCGGTGACCATGATAGTGTTTGTCCAGGTTCAACTCCAGCTATGGCTTCCCAGTGGA 175
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                                                                                                                                                        236 TCCAGCTGACCAGCTGCGTGTGTTTTTGCCGGGAAGGAGCTTCCGAATCACCTGACGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOWARD P. SHARROCK, REBERT H.; CHRISTENSEN, ALAN H.; HERSHEY, HOWARD P.; SHARROCK, REBERT A.; SULLIVAN, THOMAS D.
TITLE OF INVENTION: PLANT UBIOUTIN PROMOTER SYSTEM
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/28/296,268
FILING DATE: 25-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 191,134
FILING DATE: 11-JUN-1993
APPLICATION NUMBER: 197,496
FILING DATE: 11-JUN-1993
APPLICATION NUMBER: 670,496
FILING DATE: 11-JUN-1993
APPLICATION NUMBER: 194,824
FILING DATE: 12-MAY-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 57.2; DB 6; Length 3e Fred. No. 1.3e-05; 0; Mismatches 119; Indels
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52.0%;
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Best Local Similarity 52.00
Matches 128; Conservative
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Patent No. 5510474
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128 CATGATAGTGTTGTCAGGTTCAACTCCAGGTATGGCTTTCCCAGTGGAGGTCGATTCTGA 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 CATGOAGATOTTOGTAAAGACCCTOAGGGTAAGAGOATCACCCTTGAGGTGGAGTOTTO
                   Improved methods for transforming Phaffia and recombinant DNA for use therein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                i.7%; Score 56.6; De 4; Length 570;
53.2%; Pred. No. 5.7e-06;
tive 0; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                (EPC
                                                                                                                                                                                                                                                                                                                                                Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product = "PRoDNAl0
                                                                                                            2: Morrison & Foerster lip
2000 Pennsylvania Avenue, N.W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFPLICATION NUMBER: EP 95203620.0
FILING DATE: 22-DEC-1995
APPLICATION NUMBER: BF 9620943.7
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: E. Victor Domano: REGISTRATION NUMBER: 35,492
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       SCHWARD PAGENTE KALEASE #..U. A PELICATION DATA PPLICATION DATA PPLICATION NUMBER: US/05/091.725 FILLING DATA: 23-EEC.1996 PRIOR APPLICATION DATA.
                                                                                                                                                                                                      COUNTRY: United States of America 2019: 20006-1889 CMRUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
CCEMPUTER: IBM PC compatible
OPERATER: PC 2004/S-008
SCFTWARE: Patentin Release #1.0.
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                           TITLE OF INVENTION: an NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 24..500
; OTHER INFORMATION:
US-09-091-725-24
                                                                                                                         STREET: Zovo
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APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
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MCLECULE TYPE:
HYPOTHETICAL: N
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PESULT 9 US-08-505-486-93

Sequence 24, Application US/09091725 Patent No. 6329141

RESULT 8 US-09-091-725-24

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APPLICANT: WILLIAM BELKNAP
TITLE OF INVARION: UBIJUITIN-LYTIC PEPTIDE FUSION GRNE CONSTRUCTS, PROTEIN PRODUCT
WINDER OF SOCIENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSES: STEVEN J. HULTOUIST
ADDRESSES: STEVEN J. HULTOUIST
STREET: 200 PARK DRIVE, SUITE 210
STREET: 200 PARK DRIVE, SUITE 210
STREET: 200 PARK DRIVE, SUITE 210
STREET: ADDRESSERVEN TRIANGLE PAPK
STATE: NORTH CAROLINA
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                                                                                                                                                                                                                                                                                                                                          CONFUTER READABLE FORM:
MEDIUM TYPE: DISKETTE:
COMPUTER: APPLE MACINTOSH
OPERATING SYSTEM: MACINTOSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JMBER: US/08/801,028
19-FER-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE.
SOFTWARE.
SOFTWARE.
SOFTWARE.
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,476
FILING DATE: 04-20-94
APPLICATION NUMBER: 08/225,476
FILING DATE: 04-39-94
APPLICATION NUMBER: 08/33,620
FILING DATE: 06-94
APPLICATION NUMBER: 08/149,431
FILING DATE: 11-08-93
APPLICATION NUMBER: 08/149,491
FILING DATE: 11-08-93
APPLICATION NUMBER: 08/149,491
FILING CATE: 11-08-93
APPLICATION NUMBER: 08/149,899
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SOMESS: DOUBLE STRANDED
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TELEPHONE: (919)990-9531
TELEFAX: (919)990-9532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cuery Match
Best Local Similarity 52.6%
Matches 123, Conservative
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                                                                                                                                                                                                                                                           STATE: N
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                                                                                                                   UBIQUTIN-LYTIC PEPTIDE FUSION GENE
CONSTRUCTS, PROTEIN PRODUCTS DERIVING THEREFROM, AND
METHODS OF MAKING AND USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 TCCAGCTGACCAGCTGCGTGTGATTTTTGCCGGGAAGGAGCTTCCGAATCACCTGACGCT 295
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                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 2004
COMPUTER READABLE FORM:
MEDIUM TYPE: LISKETTE, 3.5 INCH, 1.4 MB STORAGE
CMEDIUM TYPE: LEM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                           ADDRESSEE: RCTHWELL, FIGG, ERNST & XURZ STREET: 555 Thirteenth Street N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
SOFTWARE:
SOFTWARE:
WordPerfect 5.1.4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,486
FILING DATE: 21.4UL-1995
CLASSIFICATION: 536
PROR APPLICATION 536
PROR APPLICATION 536
PROR APPLICATION: 536
APPLICATION S36
ATTORNEY AGENT 1NFORMATION:
NAME: WALKER, BARBARA W.
REGISTRATION NUMBER: 35,400
REFERCE/POCKET NUMBER: 35,400
REFERCE/POCKET NUMBER: 2093-117A
TELEFHONE: (202) 783-6040
         Sequence 93, Application US/08505486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INCRMATION (202) 83-6040 TELEFAX: (202) 783-6040 TELEFAX: (202) 783-6031 INCRMATION FOR SEQ ID NO: 93: SEQUENCE CHARATERISTICS: LENGTH: 1154
                                                                                    APPLICANT: Jesse M. Jaynes
TITLE OF INVENTION: UBIQUIIN
TITLE OF INVENTION: CCNSTRUC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 98
CORRESSPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
DESCRIPTION: GENOMIC ENA
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Best Local Similarity 52.6
Matches 123, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LINEAR
                              Patent NO. 5955573
GENERAL INFORMATION:
APPLICANT: Jesse
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                                                                                                                                                                                                                                                        ADDRESSEE:
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-08-801-028-93
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                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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1388 TGCCGACTACAACATCCAGAAGAGTCACCACTCTCCTGTSCTCCGTCTCCG 1141

RESULT 11 US-09-340-154-93

Sequence 93, Application US/08801028 Patent No. 6018102 GENERAL INFORMATION APPLICANT: JOAN GARBARING APPLICANT: JESSE M. JAYNES

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APPLICANT: Belknap, William Title Febride Fusion Gene Constructs. Protein Products Title OF INVENTION: Ubiquitin Lytic Peptide Fusion Gene Constructs. Protein Products File Reperence: 2001-14 Threfrom Therefrom 12 Making and Jeing Same File Reperence: 2001-14 Threfrom 12 Making and Jeing Same CURRENCE: 2001-14 Threfrom Marses: 120-01-14 File Reperence: 2001-14 File Reperence: 2001-14 File Reperence: 2001-02-19 File Republication NUMBER: US 38/601,026 File Republication NUMBER: US 38/601,026 File Republication NUMBER: US 301-02-19 File Republication NUMBER: US 301-02-10 Septime File Republication NUMBER: US 301-02-10 Septime File Republication Number: Security NUMBER: Settlin Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     968 GGTTGAGTCTTCCGACACCATCGACAATGTCAAAGCCAAGATCCAGGAGAAGAGAT 1627
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CONSTRUCTS, FROTEIN PROBUCTS DERIVING THEREFROM, AND
METHODS OF MAKING AND USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: Jbi3-ubiquitin insert sequence
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GENERAL INFORMATION:
APPLICANT:
TITLE CF INVENTION: UBIOJITIN-LYTIC PETITLE OF INVENTION: CONSTRUCTS, PROTEIL
TITLE OF INVENTION: CONSTRUCTS, PROTEIL
TITLE OF INVENTION: METHODS OF NAKING A
COMPUTER READABLE FORM:
MEDIJM TYPE: Florgy disk
COMPUTER: IRW PC compatible
OPERATING SYSTEM: PCOS/MS-FOS
SCFTWARE: WORDERECT 5.14
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: CA/279,472
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LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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PCT-US95-09338-93
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                                                                                                          APPLICANT: Jesse M. Jaynes .
TITLE OF INVENTION: USEQUITH-LYTIC PEPTIDE FUSION GENE
TITLE OF INVENTION: CONSTRUCTS, PROTEIN PRODUCTS DERIVING THEREFROM, AND
TITLE OF INVENTION: METHODS OF MAKING AND USING SAME
NUMBER OF SECURNOS: 93
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 TCCAGCTGACCAGCTGCGTGTGATTTTTGCCGGGAAGCTTCCGAATCACCTGACGGT 295
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Best Local Similarity 52.6%; Pred. No. 1e-05;
Matches 123; Conservative 0; Mismatches 11; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER REALABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.4 MB STORAGE
COMPUTER: IEM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION OATA:
PRIOR APPLICATION NUMBER: (28/505,486
FILING DATE: 21-JUL-1995
APPLICATION NUMBER: U.S. 08/279,472
FILING DATE: 22-JUL-1994
ATTCRNEY/AGENT INPORMATION:
NAME: WALKER, BARBARA W.
REGISTRATION NUMBER: 35,400
REFERENCE/DOCKET NUMBER: 2093-117A
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                               STREET: 555 Thirteenth Street N.W. CITY: Washington STATE: D.C.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/340,154
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S-09-482-6118-93
Sequence 93, Application US/094826:18
Parent No. 6448391
GENERAL INFORMATION:
APPLICANT: Garbarino, Joan
       Sequence 93, Application US/09340154
Patent No. 6084156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE STRANDED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: GENOMIC DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                      GENERAL INFORMATION:
APPLICANT: Jesse
                                                                                                                                                                                                                                                                                                                                                                                                                                D. C.
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Length 1154;

Score 56.4; JB 5; Pred. No. le-05;

Query Match Best Local Similarity

GENOMIC DNA

DESCRIPTION:

PCT-13895-09336 93

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Sequence 92, Application US/08505486
| Patent No 695573 | GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL PRODUCTS, PROTEIN PRODUCTS DENIVING THREFFOX, AND TILLE OF INVENTION GENERAL PROGUENCES 96 CORRESPONDENCE ADDRESS: 96 CORRESPONDENCE ADDRESS: NOTHWELL, PIOG, ERNST & KURZ STREET: 555 Thirteenth Street N.W. COLTY: Washington STATE: D. C. COUNTRY: USA ZEE: 20024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iii; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.4 ME STORAGE
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPCLOGY: LINEAR
NOBECUDE TYPE:
ESCRIPTION: GENOMIC DNA AND OTHER NUCLEIC ACID
US-06-505-546-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.7%; Score 56.4; DB 2;
52.6%; Pred. No. 1.1e-05;
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Job time : 158 secs
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CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/505,486
FILING DATE: 21.4UL-1995
CLASSIFICATION: 836
FRIOR APPLICATION: 836
FRIOR APPLICATION: 836
FRIUND CATES: 2.2.01L-1994
CLASSIFICATION NUMBER: U.S. 08/279,472
FILING DATE: 2.2.01L-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: WALKER, BARBARA W.
REGISTRATION NUMBER: 25,406
REGISTRATION NUMBER: 2093-117A
TELECOMMUNICATION INFORMATION:
TELECHEOS: (202)783-6046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE STRANDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202)783-6040
TELEPAX: (220)783-603.
INFORMATION FOR SEC 12 NO. 92:
SEQUENCE CHARACTERISTICS.
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Best Local Similarity 52.6
Matches 123: Conservative
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OPERATING SYSTEM:
SOFTWARE: WordPerf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
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TITLE OF INVENTION: UEFQUITIN-LYTIC PEPTIDE FUSION GENE
TITLE OF INVENTION: CONSTRUCTS, PROTEIN PRODUCTS DERIVING THEREFROM, AND
TITLE OF INVENTION: METHODS OF MAKING AND USING THE SAME
NUMBER OF SEQUENCES: 98
COMPUTER READABLE FORM:
MEDIUM TYPE: FLODRY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 gescogorgancarsanasteringreascricaacterascriteceascas 175
                                                                                                                                                                                                                                               906 CCTCCAGGCGAAGATGCAGATCTTCGTGAAGACCTTAACGGGGAAGACGATCACCCTAGA 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 CCGCCCGGTGACCATGATAGTGTTGTCAGGTTCAACTCCAGCTATGGCTTCCCAGTGGA 175
                                                                                                                                                                                                                                                                                                      176 GGTCGATTCTGACACCAGCATCTTGCAGCTCAAGGAAGTGGTTGCTAAGCGACAGGGGGT 235
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                                                                                                                                                                                                                                                                                                                                           176 GOTCGATTCTSACACCAGCATCTTGCAGCTCAAGGAAGTGGTTGCTAAGCGACAGGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1088 ISCCGACTACAACATCCAGAAGSAGTCAACTCTCCATCTCGTGCTCCGTTCTCC 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 TCAAAACTGTGACCTGGAACAACAGGTATTGTACACATAGTACAGAGACCACG 343
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                                                                                                                                                           0; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FCT/US95/09339 FILMS DATE: 2-24L1994 PRICR APPLICATION DATA: APPLICATION NUMBER: 08/279,472 FILMS DATE: 2-2405.1994 INFORMATION FOR SEQ ID NO: 93: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Sequence 93, Application PC/TUS9509339 , GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COTPARIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1*
CURRENT APPLICATION DATA:
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STRANDEDNESS: DOUBLE STRANDED
TOPOLCGY: LINEAR
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Sequence Sequence Sequence Sequence Sequence Sequence

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RESULT:

(S-09-78-548-3

(S-09-78-548-3

) Sequence 3, Application US/09785548

) Patent No. US20201557741

| Patent No. US20201557741

| APPLICANT: AVENTIS PHARMATION: COMPOSITIONS. THAT CAN BE USED FOR REGULATING THE ACTIVITY OF TITLE OF INVENTION: COMPOSITIONS. THAT CAN BE USED FOR REGULATING THE ACTIVITY OF TITLE OF INVENT APPLICATION UNMBER: US/09/785,548

| CURRENT APPLICATION UNMBER: US/09/785,548

| CURRENT APPLICATION OF SEQ. ID NCS: 46

| SCOTTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCCAGACTGCCTGGAACCAGAGCTGAATTTTTCTTTAAATGTGGAGCACACCCAACCT 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 CAGGTAGATCAATCTACAACAGCTTTTATGTGTATTGCAAAGGCCCCTGTCAAAGAGTGC
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hes 73; Indels
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US-10-199-572-501
US-10-26-167-158
US-10-26-167-158
US-10-187-749-201
US-10-186-14-7-201
US-10-186-14-7-201
US-10-186-14-7-201
US-10-186-14-7-201
US-10-186-14-7-201
US-10-186-14-7-201
US-10-186-14-7-201
US-10-186-14-7-201
US-10-186-14-7-201
US-10-186-14-869-201
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Pred. No. 6.6e-
0; Mismatches
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Best Local Similarity 84.0
Matches 384; Conservative
     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LUCATION: (1); (471)
US-03:785-548-3
      NAME/KRY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Appli
                                                                                                           / Search time 599 Seconds
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14573.058 Million cell updates/sec
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                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications NA:*

| cgn2 6/ptodata/2/pubpna/US07 PUBCCMB.seq:*
| cgn2 6/ptodata/2/pubpna/DSC NEW PUB.seq:*
| cgn2 6/ptodata/2/pubpna/USC NEW PUB.seq:*
| cgn2 6/ptodata/2/pubpna/USC NEW PUB.seq:*
| cgn2 6/ptodata/2/pubpna/USOF PUBCCMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compagen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-785-548-3
US-09-864-76-3503
US-09-814-353-5846
US-09-814-353-12127
US-09-814-353-12127
US-09-815-824-3
US-09-816-35-8511
US-09-918-935-35452
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US-09-946-374-51
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Maximum Match 100%
Listing first 45 summaries
                                                                               - nucleic search, using sw model
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seg length: 2000030000
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Match
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Perfect score:
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Sequence Sequence Sequence Sequence Sequence Sequence

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Gaps

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Length 471;

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PRESENT NO. USESSEQUESTATION:

APPLICANT: Renn, Sharron G.
APPLICANT: Chen. Sharron G.
APPLICANT: Chen. Sharron G.
APPLICANT: Chen. Sharron G.
TITLE OF INVENTION: HUMAN GENONE-DERIVED SINGLE EXCN NUCLEIC ACID FROBES USEFUL FC
TITLE OF INVENTION: HUMAN GENONE-DERIVED SINGLE EXCN NUCLEIC ACID FROBES USEFUL FC
TITLE OF INVENTION: HUMAN GENONE-DERIVED SINGLE EXCN NUCLEIC ACID FROBES USEFUL FC
THE REPEAR TILING DATE: 200-02-04
PRICE APPLICANTION NUMBER: US 60/180,312
PRICE APPLICANTION NUMBER: US 60/180,315
PRICE FILING DATE: 200-02-04
PRICE FILING DATE: 200-02-05
PRICE FILING DATE: 200-02-03
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                                                                                  N: MAP TO ALC35697.18
N: EXPRESSED IN PLACEVIR, SIGNAL = 0.68
N: EXPRESSED IN HELA, SIGNAL = 0.76
N: EXPRESSED IN HELA, SIGNAL = 0.94
N: EXPRESSED IN HELA, SIGNAL = 0.94
N: EXPRESSED IN BTAL LIVER SIGNAL = 0.63
N: EXPRESSED IN BRAIN, SIGNAL = 0.91
N: EXPRESSED IN AULT LIVER SIGNAL = 0.77
N: EXPRESSED IN HEART, SIGNAL = 0.77
N: EXPRESSED IN HEART, SIGNAL = 0.77
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Patent No. US20020848763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                  OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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CTHER INFORMATION:
OTHER INFORMATION:
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US-09-864-761-20274/c
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Matches 123;
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                                                                                                   251 CTGACAAGGAAACATCAGTAGCTTTGCACCGAACGAAATAGTCGGAACATCACTT 310
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                                                                                                                                                                                                                                                                                                             TGATCTGTTTGGACTGTTTCCACTTGTATTGTGTCACAAGACTCAACGATCGGCAGTTTG 957
   19: CCCCACACTGCCCTGGGACTAGTGCAGATTTTTCTTTAAATGTGGAGCACACCCCACCT 250
                                                                                                                                                                                                                       CASACAAGGACACGTCGGTAGCTTTGAACCTGATCACCAGCAACAGGCGCAGCATCCCTT
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us-09-830-703-1.rnpb

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PRICK FILING DATE: 2000-12-21
NUMBER CF SEG ID NGS: 22037
SEG ID NO SEG for Windows Version 4.0
SEG ID NO SEG
LENGTH: 810
                                                                                                                                                                                                                                                                                                                                                           NAME/KEY. Tisc_feature
LOCATION: 163, 165, 172, 174, 185, 18
LOCATION: 216, 222, 232, 232, 232
LOCATION: 266, 237, 291, 292, 284, 29
LOCATION: 338, 339, 341, 345, 344, 35
OTHER INFORMATION: n = A.T.C or 5
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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| Sequence 5846, Application US/09914353 |
| GENERAL INCRMATION: | APPLICANT: Incomposor, Pamela |
| APPLICANT: Incomposor, Demela |
| APPLICANT: Incomposor, Demela |
| APPLICANT: Incomposor, Demela |
| FILE OF INVENTION: INEXPISE US/09/814,353 |
| CURRENT FILING DATE: 2001-03-21 |
| PRIOR APPLICATION NUMBER: US 60/201,24 |
| PRIOR PELING DATE: 2000-05-25 |
| PRIOR FILING DATE: 2000-06-15 |
| PRIOR FILING DATE: 2000-06-15 |
| PRIOR FILING DATE: 2000-05-06 |
| PRIOR FILING DATE: 2000-05-06 |
| PRIOR FILING DATE: 2000-07-07 |
| PRIOR PRING DATE: 2000-07-07 |
| PRIOR FILING DATE: 2000-07-07 |
| PRIOR PRIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.2%; Score 103.2; DB 9; Length 140; Best Local Similarity 83.6%; Pred. No. 7.5e-19; Matches 117; Conservative 0; Mismatches 23; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEATURE:
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.68
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.68
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.76
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN HETA, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 0.63
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.73
OTHER INFORMATION: MT HIT: 917669537, EVALUE 2.00e-73
OTHER INFORMATION: BST HUMAN HIT: 9204833, EVALUE 7.30e+00
US-09-864-761-20274
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PZT/US31/00670
PRIOR FILING DATE: 2001-320
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2005-09-31
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774.203
PRIOR APPLICATION NUMBER: US 09/774.203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49127
SOFTWARE: Annomax Sequence Listing Engine vers: 3.1
SEQ ID NO 20074
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2537 ISTIAALCITICAAGGILTCITLCOTITLCGISTITTATITGITTISCILLGGIT 2596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASSULTS
Sequence 12127, Application US/C9814383
Sequence 12127, Application US/C9814383
Sequence 12127, Application US/C9814383
Sequence 12127, Application US/C9814383
GENERAL INFORMATION
APPLICANT: Lee, Obn
APPLICANT: Lee, Obn
APPLICANT: Lee, Obn
APPLICANT: Thompson, Pamela
APPLICANT: AND WEBAPY OF CYRILA
TITLE OF INVENTION: THERAPY OF CYRILA
TITLE OF INVENTION: THERAPY OF CYRILA
TITLE OF INVENTION: THERAPY OF CYRILA
TITLE OF INVENTION: AND THERAPY OF CYRILA
THERAPY APPLICANTION NUMBER: US 60/211,940
PRICE FILING DATE: 2000-06-15
PRICE APPLICANTION NUMBER: US 60/210,641
PRICE TILING DATE: 2000-06-15
PRICE APPLICANTION NUMBER: US 60/210,641
PRICE TILING DATE: 2000-06-15
                                                                                                                                                                                       468, 469, 470, 476,
534, 535, 538, 538,
600, 603, 614, 621,
645, 647, 648
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738, 739, 746,
798, 800, 805
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                                                                                                                                                                                                                                                                                                                                                                            737, 7
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123
185
641
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736,
785,
25.52
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527,
584,
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Sequence 3. Application US/0985824
Publication No. US2030166648A1
GEREAL INFORMATION:
GEREAL INFORMATION:
GEREAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THREOF
FILE REFERENCE: CL0123
FILE REFERENCE: CL0123
FURRENT APPLICATION NUMBER: US/09/855,824
CURRENT APPLICATION NUMBER: 10/09/855,824
CURRENT FILNG DATE: 201-05:16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version: 4.0
SEQ ID NO: 1
LENGTH: 143601
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                                                                                               | THAMATGIGORGCACACCCAACCICASACACATCGGTACGTTTGAACCTGATCA 60
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PUDLICATION NO. US20630166831A1
FUDLICATION NO. US20630166831A1
FUDLICATION NO. US2063031A1
APPLICANT: Line, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thise, James
APPLICANT: Thise, James
APPLICANT: THERAPY OF OVERSHIP, PREVENTION, AND
APPLICANTON: THERAPY OF OVERSHIP, PREVENTION, AND
ATTLE OF INVENTION: THERAPY OF OVERSHIP
APPLICATION NUMBER: US/09/614,353
CURRENT FILING DATE: 2000-03-27
PRICE APPLICATION NUMBER: US 60/191,031
PRICE APPLICATION NUMBER: US 60/191,031
PRICE FILING DATE: 2000-03-27
PRICE FILING DATE: 2000-03-27
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                                                               754 TINAATGIGGAGGACACCCAACCICAGACAAGGACACGICGGIAGCITIGAACCIGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2413 TCTGCATATCTGCTCCGTCCTGCTGTTAAGCCCCAGGGAGCCCCATCCACCCAGTGGT
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      Gaps
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Bost Local Similarity 56.9%; Pred. No. 2.7e-05;
Marches 115; Conservative 0; Mismatches 87;
         Mismatches
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) DOCATION: (1) [1.1 (143601)
OTHER INPORMATION: n = A.T.C or G
0S-09-855-624-3
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      Conservative
                                                                                                                                                                              814 CCAGC 818
                                                                                                                                                                                                                                       61 CCAGC 65
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CRGANISM: Human
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US-09-814-353-18511
      . 69
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      Matches
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APPLICANT: SHOSHAW, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINEX. List
APPLICANT: List
APPLICANT: MINEX. List
APPLICANT: List
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2657 CATATAGANATGAJGTTATCTTGTGGTGTGAGGAAAGGCCAGCTGGCCTAAGTTCACA 2714
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534, 535, 536, 538,
600, 603, 614, 621,
645, 647, 649
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243, 266,
330, 333,
389
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// ICCATION: 649, 659, 663, 689, 690, 691, 692, 696, 697, 696,

// ICCATION: 712, 721, 723, 733, 734, 736, 736, 738, 739,

// ICCATION: 752, 754, 767, 768, 777, 783, 784, 785, 796, 798, 800,

// OTHER INFORMATION: n = A/T/C or G
                                                                                                                                           2.0%; Score 65.4; DB 12; Length 810;
55.6%; Pred. No. 1.4e-07;
tive 0; Mismatches 79; Indels 0;
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SOFTWARE: FastSEQ for Windows Version 4.6
SEQ ID NO 12127
LENGTH: 810
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Publication No. US20330165843A1
GENERAL INFORMATION:
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Best Local Similarity 55.6'
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / TYPE: DNA
: OPGANISM: Mus musculus
US-09-908-975-26043
                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-908-975-26343
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126 ACCATGATAGTGTTTGTCAGGTTCAACTGCAGCTATGGCTTCCCAGGGGGGGTCGATTCT 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 agtgacaccattgagaatgicaaagccaaaattcaagacaaggaggtatccoacctgac 156
        187 CAGCAGCGTCTGATATTTGCCGGCAAACAGCTSGAGGATGGCGGGACTGTTGTGTGAGACTAC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 AACATGCAGATCTTTGTGAAGACCCTCACTGGGAAAACCATCACCCTTGAGGTCGAGGCC 96
                                                           3.06. GACCTGGAACAACAGAGTATTGTACACATAGTACAAGAACCACGGAGGAGGAAGTGATGA 3.64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 AACATOCAGAAAGAGTOCAGCOTSCACCTGSTGTTGCSCCTGCGAGGTGGCATTATTGA 275
                                                                                                          247 AACATCCAGAAAGAGTCCACACCTGCAGCTTGCGCCTGCGAGGTGCCATTATTGA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 473;
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Sequence 20526, Application US/0901995

Sequence 20526, Application US/0901995

Publication No. US20030773623A.

GENERAL FROEMATION:
APPLICANT: Hyseq, Inc.
ITLE DT INVENTION: NOVEL NUCLEIC ACID SECUENCES OSTAINED
ITLE DT INVENTION: PROM VARIOUS CONA LIBRARIES
FILE REPRENCE: 20411-756
CURRENT PELLORION: FROM VARIOUS CONA LIBRARIES
CURRENT FILING DATE: 2001.07-20
PRIOR PLING DATE: 1999-01.00
PRIOR FILING DATE: 1999-01.00
PRIOR FILING DATE: 1999-01.00
SEQ ID NOS: 18004
SCFTWARE: FASESED for Windows Version 3.0
                                                                                                                                                                                                                                                                                                               APPLICATION THYSE OF THE OF THE OF THE OF TWENTION: NOVEL WICELC ACID SEQUENCES CENTAINED TITLE OF TWENTION: NOVEL WICELC ACID SEQUENCES CENTAINED TITLE OF TWENTION: PROM VARCOUS CENTA LIERARIES CURRENT APPLICATION NUMBER: 13/09/218,995
CURRENT RILING DATE: 200.073
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38654
SOTTWARE: FasteEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53.1%; Pred. No. 3.8e-06;
Matches 127; Conservative 0; Mismatches 112; Indels
                                                                                                                                                                                                                                            ; Sequence 23749, Application US/09918998; Publication No. US20030073623A1; GENERAL INFORMATION:
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| LOCATION: (1) | ... (5.55)
| OTHER INFORMATION: n = A.T.C or G
| US-09-918-995-20526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 GACACCAGGATCTTGCAGGTCAAGGAAGTGGTTGCTAAGCGACAGGGGGTTCCAGCTGAC 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CONA LIBRARIES
FILE REPERBACE 20411-756
CURRENT APPLICATION NUMBER: US/09/318,995
CURRENT FILING DATE: 2001-07-30
PRIOR PLILING DATE: 2999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASESED for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.9%; Score 60.4; DB 12;
Best Local Similarity 61.4%; Pred. No. 2.7e-06;
Matches 97; Conservative 0; Mismatches 61;
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PRIOR APPLICATION UNMBER: US 60/211,940
PRIOR FILING DATE: 2000-6-15
PRIOR FLING DATE: 2000-05-17
PRIOR FILING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR FILING DATE: 2000-12-21
NUMBER: OF SEQ 13 NOS: 2237
SOFTWARE: FASTERO FOR WINDOWS VERSION 4.0
SOFTWARE: FASTERO FOR WINDOWS VERSION 4.0
SEQ 1D NO 18511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 35452, Application US/39918995
Publication No. US20030373623A1
GENERAL INFORMATION:
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LOCATION: (1)...(440)

OTHER INFORMATION: n = A,T,C or G

US-09-918-995-35452
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
) ORGANISM: Homo sapiens
US-09-814-353-18511
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: PROPOSICION FOR THE REFERENCE: PROPOSICION TO BROWN NUMBER: US/09/946,274 CURRENT FILING DATE: 2001-09-04
377 GATGIGATGAACCCCCCAGAACCCCTGGGA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRICK APPLICATION NUMBER, 60/28723
PRICK APPLICATION NUMBER, 60/28723
PRICK APPLICATION NUMBER, 60/08749
PRICK APPLICATION NUMBER, 60/08750
PRICK APPLICATION NUMBER, 60/08675
PRICK APPLICATION NUMBER, 60/08671
PRICK APPLICATION NUMBER, 60/08676
PRICK APPLICATION NUMBER, 60/08676
PRICK APPLICATION NUMBER, 60/08956
PRICK APPLICATION NUMBER, 60/08956
PRICK APPLICATION NUMBER, 60/08956
PRICK APPLICATION NUMBER, 60/08967
PRICK APPLICATION NUMBER, 60/08968
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Grimaldi, Christopher J.
Gurney, Austin I.
Hillan, Kenneth J.
                                                                                                                                                                       Sequence 51, Application US/09946374 Publication No. US23030073129A1 GENERAL INFORMATION:
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Roy, Margaret Ann
Smith, Victoria
Stewart, Timothy A.
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Baton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
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Williams, P. Mickey
Wood, William I.
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Botstein, David
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-06
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 TIGAGAATGTCAAAAGCCAAAATTCAAGACAAGGAGGGTTCCCACCTGACCAGCAGCAGCGGGC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 TGATTITIGCCGGGAAGGAGCTTCCGAATCACCTGACGGTTCAAAACTGTGACCTGGAAC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 "GATATTTGCCGGCAAACAGCTGGAAGATGGACGTACTTTGTCTGACTACAATATTCAAA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 AACAGAGTATTGTACACATAGTACAGAGACCACGGAGGAGAAGTCATGAAACAAATGCAT 375
                                                                                                                                                                                                                                                                                                      113 AGTGACRCCATTGAGAATGTCAAAAGCCAAAATTCAAGAAGGAAGGGGTATCCCACCTGAC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 TOTITICICAGGITICAACTCCAGCTATGGCTTCCCAGTGGAGGTCGATTCTGACACCAGCA 195
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                                                                                                                                                 126 ACCATGATAGTGTTTGTCAGGTTCAACTCCAGCTATGGCTTCCCAGTGGAGGTCGATTCT 185
                                                                                                                                                                                                       55 AACATGCAGATCTTTGTGAAGACCCTCACTGGCAAAACCATCACCCTTGAGGTCGAGCCC :14
                                                                                                                                                                                                                                                                186 GACACCAGCATCTTGCAGCTCAAGGAAGTGGTTGCTAAGCGACAGGGGGTTCCAGCTGAC 245
                                                                                                                                                                                                                                                                                                                                                                                  246 CAGCTGCGTGTGTTTTTGCCGGGAAGGAGCTTCCGAATCACCTGACGGTTCAAAACTGT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                 175 CAGCAGCGICIATATITGCCGGCAAACAGCIGGAGGAIGGCCGCACTCICTCAGACIAC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 AACAJCCAGAAAGAGTCCACCCTGCACCTGGTGTTGCGCCTGGAGGTGGCGCTTATAA 293
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                            Ouery Match 1.8%; Score 59.8; DB 11; Length 505; Best Local Similarity 53.1%; Pred. No. 4e-06; Matches 127; Conservative 0; Mismatches 112; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
1.8%; Score 59.8; DB 10; Length 3
Best Local Similarity 51.3%; Pred. No. 7.6e-06;
Matches 139; Conservative 0; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: 77 HOUDIFY CYS-APO A-1 plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 45, Application US/09987107
Patent No. US20020156007A1
APPLICANT: GRAVERSEN, Jonas
APPLICANT: GRAVERSEN, Jonas
APPLICANT: MORETRUP, SOTER
TILLE OF INVENTION: APOLIPOPROTEINS ANALGGUES
FILE REFERENCE: GRAVERSENIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 66/264,022
PRIOR PILING DATE: 2001-01-26
PRIOR PILING DATE: 2001-01-25
PRIOR PLING DATE: 2001-01-25
PRIOR PLING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2001 01682
PRIOR PLING DATE: 2000-11-15
PRIOR PLING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 61.8%; Pred. No. 1.4e-05;
Matches 94; Conservative 0; Mismatches 58; Indels 0;
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 170
SEQ ID NO 51
LENGTH: 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2657 CATATAGAAATGATGTTATCTTGTGGTGTGAG 2688
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                                                                                               / TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-063-735-51
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Publication No. US20030138982A1
GENERAL INPORMATION:
APPLICANT: Eaton, Oan L.
APPLICANT: Eaton, Oan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerifsen, Mary E.
APPLICANT: Gerifsen, Mary E.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Wood, Milliam I.
APPLICANT: Wood, Milliam I.
APPLICANT: Matanabe, Colin K.
APPLICANT: Matanabe, Colin K.
APPLICANT: ACTION THE SAME
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFRENCE: PAISORICI
CURRENT APPLICANTION NUMBER: US/10/663,735
CURRENT APPLICANTION DATE: 2002-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Panois. Nicholas F.
TITLE OF INVENTION: Serreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2830PLC54
CURRENT APPLICATION UNMER: US/10/G15,387A
CURRENT FILING DATE: 2001-12-12
Prior Application removed - See File Wrapper or Paim
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 5: 477
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       2657 CATATAGAAATGATGTTATCTTGTGGGTGTGAG 2688
                                               1580 AGTGATGAGAGGTGGTGTTTTAAGGAGGAG 1549
                                                                                                                                                                   Sequence 51, Application US/10015387A Publication No. US20030135034A1 GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul J
Grimaldi, Christopher J
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Fong, Sherman
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Hillan, Kenneth J.
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APPLICANT: Borstein, David
APPLICANT: Desnoyers, Juc
APPLICANT: Eaton, Dan i.
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; ORGANISM: Homo sapiens
US-10-015-387A-51
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US-10-063-735-51/c
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APPLICANT:
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ر. دن	aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	mber of hits satisfying chosen parameters: DB seq length: 0 DB seq length: 2000000000 Cessing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : EST: 1: em_estba:* 2: em_esthum:* 4: em_esthum:* 5: em_estrun:* 6: em_estrun:* 7: em_estrun:* 9: 9p_estl:* 10: 9p_es	12: gp est3: 13: gb_est4: 14: gb_est5: 15: em_estfun:*	16 em_estcm: * 17 em_gss_fun: * 19 em_gss_fun: * 19 em_gss_fun: * 19 em_gss_fun: * 20 em_gs_fun: * 20 em_gss_fun: * 20 em_gs

us-09-830-703-1.rst

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strand cDNA was prepared with the primer adapter of sequence [5] dAGAGAGATTCHOGAGTTAATTAAATTAATTCCCCCCCCCC 1], cDNA was cleaved with BamHI and Xbol. cDNA of size corprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript XS:*! after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI. Bost: DALOB.
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/db_xref="MG1:1355296"
/db_xref="MG1:1355296"
/db_xref="MG1:1355296"
/db_xref="MG1:1355296"
/cransiation="MRVCLPSTTSGDTSAYLLPPJJLSPRESPHPPSGPTDRAIHTHQ
DSGQVRKGQU-A"
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Korno, H., Akiyama, J., Nisfi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsuroto, H., Sakaguchi, S., Itogami, T., Kashwagi, K., Yaliwaka, S., Itoue, K., Togawa, Y., Izawa, M., Ohara, E., Washiki, M., Yonda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Marsurta, S., Kawai, J., Ckazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Sequencing pipeline with 384 multicapillary sequencer analysis (RISA). system--384-format
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Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand CDNA was primed with a primer [5] GAGAGAGAGAGACATCTTTTTTTTTTTTTTV 3], CDNA was an expected by using trehalose thermo-activated reverse transcriptise and subsequently enriched for full-length by cap-trapper. Second
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Analysis of the mouse transcriptome based on functional annotation of 60,777 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2182)
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602692618F1 NIH_MGC_92 Homo saptens CENA clone IMAGE:4824892 5'',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hono.
1. ibases i to 910;
NIE-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Sobert Strausberg, Ph.D.
Email: Gagbs-rimmal.uth.gov
Tissue Producterent: uth.gov
Tissue Producterent: Middle Palkovits, M.D., Ph.D.
Tissue Producterent: Middle July Brownstein (HHGRI), Shira
CDNA Library Presponding (R.KEN
CDNA Library Arrayed by The T.M.A.G. Consortium (LiML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NGC clone distribution information can be
found through the I.M.A.G.E. Consortlut/LiNL at:
Plate: LiaMHG737 row: c column: SS
                                                                                           725 ATGAGGGGCACCTTTGGTTTTGGACTCTGTAGAAGCCATSAGTGAGGTGGGAASTG-TTT
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Normalization and subtraction of cap-trapper-selected CDNAs to prepare included the CDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2003)
RIKEN streepared Sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequence. Genome Res. 10 (11), 1757-1771 (2003)
Computer-based methods for the mouse full-length countries concurred to the construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2011), CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Genome Encyclopedia Project of Genome Exploration Research Genome Encyclopedia Project of Genome Exploration Research Genome Encyclopedia Project of Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
Fax: 81-45-503-9222
Fax: 81-45-503-9212
Fax: 81-45-503-9216
Fax: 81-45-503-9216
Fax: 81-45-503-9216
MGChi.C. Aizawa.K. Akimura,T., Arakawa.T., Carninci,P., Fukuda Adchi.C., Aizawa.K., Akimura,T., Arakawa.T., Hori,F., Imcrani.K., Shiisi,Y., Itoh,W., Kagawa.T., Kawa.J., Kojima,Y., Kondo,S., Konno,H., A., Koya,S., Miyazaki.A., Murata,M., Norura,K., Murata,M., Norura,K., Nomazaki.R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waxi,K., Waxahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

18.2%; Score 590.8; DB 14; Length 963;
Best Local Similarity 95.3%; Pred. No. 1.le-47;
Matches 663; Conservative 0; Mismatches 27; Indels 6; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
/stain="CS7BL/CS7BL/CJ"
/db_xref="taxon:1000"
/clone="4930538K15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="testis"
/dev_stage="adult"
/lab_host="SOLR"
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Exaryota Mecazoa Chordata Craniata Vertebrata; Euteleostomi;
Bases 100 453)

Sodontia; Scinceria; Sciurognath; Muridae; Murinae; Mus.
Bases 100 453)

Najalo; Dosato, M. Sasto, R. Suzuki, H. Yamanaka, I. Kiyosawa, H. Yadado, J. Osato, M. Sasto, R. Suzuki, H. Yamanaka, I. Kiyosawa, H. Yadado, J. Osato, M. Bases 100 48, J. Scinralla, M. Rangin, A. Marsuda, H. Batalov, S. Beisel, K. W. Bake, J. M. Rangin, A. Marsuda, H. Batalov, S. Beisel, K. W. Bake, J. M. Rangin, T. Grindler, G. Forrest, J. Consins, S. Dalla, B. Hill, P. J. Burto, C. Hura, J. A. J. Bake, J. M. Rangin, T. W. Pietcher, C. Forrest, J. L. E. Cousins, S. Dalla, M. Rangin, T. W. Pietcher, C. Forrest, J. Consins, S. Dalla, M. Kawasawa, Y. Wedcher, C. Forrest, J. M. Kangi, H. Kawasawa, Y. Wedcher, C. Forrest, J. M. Kangi, H. Kawasawa, Y. Wedcher, C. Forrest, J. M. Kangi, H. Kawasawa, Y. Wedcher, C. Forrest, M. Mittig, E. D. Kanai, A. Kangi, H. Kawasawa, Y. Wedcher, C. Forrest, J. W. Magashima, T. Wamata, K. Warchon, L. Warchon, L. Werter, G. C. Berter, G. Forrest, M. Watana, M. Werasi, T. Reed, J. C. 
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Saboratory for Genome Exploration Research Group, RIKEN Genomic Saboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GEC). Yokohama Institute
Sciences Center (GEC). Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Submiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-6045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9226
                                                                                                                                                                                                                                       BYS96928

BYS96928 RIKEN full-length enriched, adult inner ear Mus musculus CDF clone F930102Kl3 3', mRNA sequence.

BYS56928
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943 GAGCCC 848
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Sakaraki, V. Ratuno, M., Rasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikardo, I., Osato, M., Saitor, W., Nogami, M., Schonben, C., Fyrosawa, H., Sagork, M., Sakaraki, K., Hordon, C., Chordan, C., Coston, M., Saldare, M., Kanspin, A., Buike, C., Hume, D.A., Cuackenbush, J., Schrimlian, K., Kanspin, A., Matsuda, H., Batalov, S., Beraki, D., Erazor, C., Hume, D.A., Corbani, C., Coussin, S., Daster, D., Erazor, C., Corban, C., Corres, S., Gaster, M., Biake, D.A., Bradi, D., Hilli, C., Hilli, C., Corban, C., Corpin, S., Congh, J., Strimond, S., Gaster, D., Marsin, C., Corban, C., Gaster, C., Corban, C., Congh, J., Strimond, S., Guster, C., Missawa, M., Kurochkin, I. V., Lee, V., Lennard, B., Lyons, K., Major, C., Corban, C., Corban, C., Corban, C., Congh, J., Strimond, A., Kurochkin, I. V., Lee, V., Lennard, B., Lyons, C., Congh, J., Marsis, C., Corban, C.,
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Marm. Genome 12, 67:-677 (2001)

Normalization and Subtraction of Sapirapper-Selected cDNAs to preare [all-length CDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1550 (2000)

RIKKN integrated sequence analysis (3KSA) system-1384-format sequencing pipeline with 384 multicaphilary sequencer. Genome Res. 10 (11), 157-171 (2000)

Computer-based methods for the mouse [Mill-ength CDNA encyclopedia: real-time sequence clustering for construction of a nonrectundant CDNA library descret Ses. 11 (2), 281-289 (2011)

CDNA library was prepared and sequenced in Nouse Senome Encyclopedia: Project of Genome Exploration Research Genome Exploration Pessearch Group in Riken Genome Contrabuted to Division of Experimental Animal Research in Riken contributed to
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URL:http://genome.gsc.riken.go.jp,
Alzawa,K., Akzhurall., Arakwa,T., Carninci.P., Fukuda,S., Hirozane
Alzawa,K., Akzhurall., Arakwa,T., Carninci.P., Ronno,H., Miyazaki,A.,
T., Imocani,K., Ishii,Y., Itoh,M., Rawai,C., Konno,H., Miyazaki,A.,
Miraca,M., NakaTura,X., Nomura,K., Numazaki,R., Ohno,M., Sakai,X.,
Sakazume,N., Sasaki,D., Saco,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramaisu,M., and Hayashizaki,Y. Direct
Submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(SSC), Yskohama Institute
The Institute of Physical and Cherical Research (SIKEN)
The Institute of Physical and Cherical Research (SIKEN)
The Institute of Physical and Cherical Research (SIKEN)
Tell: 81-45-501-922
Pax: 81-45-503-9226
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Tissues were provided by Kirk W. Belsel (Boys Town National
Research Abegital Scs North 30th Giret Omaha,NE 68131 USA ) whose
Chordata, Craniata, Vertebrata, Euseleostomi,
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Flease visit our web site (http://genore.gsc.riken.go.jp)
further details.
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                                   encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001).

CDNA library was prepared and sequenced in Mouse Senome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKBN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                           prepare mouse tissues.

Tissues were provided by Kirk W. Beisel ( Boys Town National Research Hospital 555 North 30th Street Omaha,NE 68131 USA ( whose assistance we grarefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /moi_type="mgN4"
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/strain="CS7BL/6C"
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/db xef="caxon:10090"
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/tissue_type="inner ear"
/dev_stage="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"
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0; Mismatches 2; Indels
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Contact: Yoshihide Hayashizaki. Contact: Yoshihide Hayashizaki. Contact: Yoshihide Hayashizaki. Laboratory Coronome Exploration Research Group, RIKEN Genomic Sciences Center (302), Yoshihide Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Swehinochon, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel 181-45-503-922 Fax: 181-45-503-922 Fax: 81-45-503-922 Fax: 81-45-503-92 Fax: 81-45-503-9	Computer-based methods for the mouse full-longth CDNA encyclopedia real-time sequence clustering for construction of a norredundant CDNA libiary. Genome feet. 11 (21, 239.589) [2001] Please visit our web site (http://gwnome.gsc.riken.go.jp) for furiner details. PEATUPES PEATUPES PEATUPES PEATUPES 465	Chery Match Sest Local Similarity 36.6%; Fred. Mo. 1.7e-28; Matches 412; Conservative O: Mismaches 12; Indels 3; Gaps 37 4 Accadegeageaceroscreatements D: Mismaches 12; Indels 3; Gaps 38 4 Accadegraphic [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]
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sequencing pipeline with 164 multicapillary sequencer. Senome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence full-length for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cCNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science and Genome Science Laborarory in Riken Genomic Science and Genome Science Laborarory in Riken Division of Experimental Animal Research in Riken contributed to
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BY237113 RIKEN full-length enriched, adult inner ear Mus musculus cDNa Cone F930102K13 5', mRNA sequence.
BY237113.1 G1:26418305
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Mammila, Eucheria, Rodentia, Boluroghathi, Muridae, Murinae, Mus.
1. (bases 1 to 416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /issue_type="inner ear"
/dev stage="adult"
/clone lb="RikEV full-length enriched, adult inner ear"
/clone 110="RikEV full-length enriched, adult inner ear"
                                                                                                                                                                                                                                                                                                                                                                             prepare mouse fissues.

Tissues were provided by Kirk W. Reisol : Boys Town National Tissues were provided by Kirk W. Reisol Chaha, NE 68131 USA : who assistance we gratically acknowledge. Picase visit our web site intp://genome.gsc.riken.go.jp/ for further details.

Location/Qualifiers
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Pred. No. 3.6e-28;
0; Mismatches 3; Indols 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mgNA"
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/db_xref="taxon:10090"
/clone="F930028E14"
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Best Local Similarity 99.28
Matches 390, Conservative
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Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Osato, I., Osato, N., Saito, R., Mull, D. P., Bult, C., Hume, D.A., Quackenbush, J., Schiml, J.M., Manapin, A., Matsuda, H., Batalov, S., Beise, K.W., Bardt, D., Brusic, V., Chothia, C., Corbani, C., Cousnas, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Forrest, R., Sasterland, T., Grasic, V., Chothia, C., Corbani, J.E., Cousnas, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Forrest, R., Maglott, D.R., Madlin, J., Mackenzie, L., Miki, M., Magshima, T., Mumata, M., Kawasawa, Y., Kedzierski, R.M., Magshima, T., Numata, K., Okido, T., Pavan, W. J., Setou, M., Magshima, T., Numata, K., Okido, T., Pavan, W. J., Percea, G., Percovettia, J., Maglott, D.R., Maglott, D.R., Magnottias, L., Machiconni, L., McKenzie, L., Miki, M., Magshima, T., Numata, K., Okido, T., Pavan, W. J., Percea, G., Percovettias, L., Machiconni, L., Machican, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Sandelin, A., Schneider, C., Semple, C., Maner, M., Sandelin, A., Schneider, C., Semple, C., Maner, M., Yang, I., Yang, L., Yang, L.
                                                                                                                                                                                                                                                                                                                                                                                                                      BY232905
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URL:http://genome-resegec.riken.go.jp,
Ajzwa-K., Akimura,T., Arakwa,T., Carninci,P., Fukuda,S., Hirozane
Ajzwa-K., Akimura,T., Arakwa,T., Carninci,P., Konno,H., Miyazaki,A.,
Xi., Imocani,K., Sahii,Y., Itch,M., Kawal,J., Konno,H., Miyazaki,A.,
Xurata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Askazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M., and Hayashizaki,Y. Direct
Submission
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The Institute of Physical and Chemical Research (RIKEN)
17-22 Suchinco-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 11: 81-45-503-922
Pax: 81-45-503-9216
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2021).
Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2020).
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                               423 TCCAGGAGCTTGACACGAGTGGACCTG 449
                                                                                                                                                                                                                 419 TCCAGGAGCTTGACACGAGTGGACCTG 445
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MEDLINE
PUBMED
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AUTHORS
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Gaps

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usessess RIKEN full-length enriched, adult inner ear Mus musculus cDNA clone F930042F15 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCGGGGGGGCGCCAGTGCCGGTAGTCTTCGAGCCGGAGCCACCCGCCGGG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOACCATGATAGTGTTTGTCAGGTTCAACTCCAG-...CTATGGCTTCCCCAGTGGAGGTCG 180
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/tissue_type="inner ear"
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i 163 c 131 g 77 c
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                                                                                                                                                                                                                                                                                           Score 358; DB 13;
Pred. No. 2.9e-25;
C; Mismatches 20;
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Matches 394; Conservative
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Email: genome-res@gsc.riken.go.jp,
Aizawa, K., Jéprome-gsc.riken.go.jp,
Aizawa, K., Akimura, T., Azakawa, Y., Kawai, J., Konno, H., Miyazaki, A., T., Imotani, K., Ishi, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Mirata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Shizaki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M., and Hayashizaki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M., and Hayashizaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
Ine Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehizocho, Tsurumi-ku, Yokohama, Kanagawa 230-2045, Japan
Tel: 81-45-503-9222
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Tissues were provided by Kirk W. Beisel (Boys Town National Tissues were provided by Kirk W. Beisel (Boys Town National Sesearch Hospital 55S North 30th Street Omaha,NE 68131 USA ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

Location/Qualifiers
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Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA computer-based methods for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computational Analysis of Full-Length Mouse cDNAs Corpared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2011)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 2617-1620 (2000;
RIKEN integrated sequence analysis (RISA) system--384-format
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/strain="C5781/63"
/db_xref="taxon:10090"
/clone="F930102K13"
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TITLE

Edwarpotal Melazoa, Chordata, Craniata, Vertebrata, Buteleostomi)

Edwarpotal Melazoa, Chordata, Craniata, Vertebrata, Buteleostomi)

I (bases 1 to 351)

I (bases 1 to 51)

I (cato.), Salto.R., Suzuki, R., Yamadaa, I., Kiyosawa, R., Kato.L., Boro.H., Kondo.S., Nigato.I., Salto.R., Nogari, R., Schonbach, C., Kiyosawa, R., Corbori, T., Baldarelli, R., Hill, D.P., Buit, C., Hume, D.A., Corbori, T., Baldarelli, R., Hill, D.P., Buit, C., Hume, D.A., Corbori, R., Bake, J.A., Barde, D., Brusic, V., Chochia, C., Corbori, J.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Razer, C., Chochia, C., Corbori, J.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Gasterland, T., Carboldi, Garde, Gasterland, T., Carboldi, Gold, J., Gold, J., Kanaja, M., Marchonni, L., McKenzie, J., Mixi, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pettea, G., Berovsky, M., Palisi, L., Konaja, L., Konido, T., Pavan, W.J., Pettea, G., Berovsky, M., Palisi, L., Nordanian, L., Marchonni, L., McKenzie, J., Mixi, Peso, G., Serple, C., Serple, C., Sercou, Ramachandian, S., Ravasi, T., Reed, D.J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Serple, C., Sercou .M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale JR.D., Tomita,M., Verardo,R., Wagnor,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wellis,C., Wilming,L.G., Mynshaw-Borris,A., Yanagisawa JM., Yang,T., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zhimer,A., Carninci,P., Fayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura

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CB811663 404 bp mRNA linear BST 16-MAY-2003 AMGNNJC:SRP92-00216-D4-A srpb2 (10220) Rattus norvegicus cDNA clone srpb2-00216-d4 57, mRNA sequence.
                                                              507 AGTAAGAGGGATTGAGAAGCAGCCAGAGGTCCAGTTAAACCCACCTACAACAGCTTTTTC 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCTGCGTGTGATTTTTGCCGGGAAGGAGCTTCCGAATCACCTGACGTTCAAAACTGG 306
                                                                                                                                                                          241 AGCIGCGIGGATITITGCCGGAAGGAGCTTCGAATCACCTGACGGTICAAAACTGIG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 ATCTACTGCAAAGGCCCCTGCCACAAGGTCCAGGGTGGAAAGCTCCGAGTTGAGTGTGGC 626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratius norvegicus (Norway rat)
Ratius norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Veriehrata, Eureleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /moi_type="mRNA"
/db xef="daxon10116"
/clone="srpb2-00216-d4"
/close_type="prostate tissue"
/clone_lib="srpb2_10220;
/rode="weccorr pSPPF11, Site 1: Sall: Site 2: Not1; rat
prostate normalized double selected poly(A-) mRNA size
                              187 ACACCAGCATOTTGCAGGTCAAGGAAGTGCTAAGCGACAGGGGGTTCCAGCTGACC
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91.8%; Pred. No. 6.46-23;
ive 0; Mismatches 31; Indels
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Tel: 805 447-4881
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                                                                                                                                                                                                                                                             Laboratory for Genomic Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Stebhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0245, Japan Tel: 81-45-503-922
Fax: 81-45-503-922
Fax: 81-45-503-922
Fax: 81-45-503-9216
Email: genome-resages.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Alzawa, K., Akhuara, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakauura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization, and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genes. Genome Res. 1C (10), 1617-1630 (2000)

RIKEN Integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-177 (2000)

Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001).

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
,M., Sakazume,N., Sato,K., Shirakı,T., Waki,K., Kawai,J., Aizawa,X., Azakwa,T., Fukuda,S., Hara,A., Hashizume,M., Imotani,K., Ishii Y., Itoh.Y., Kagawa,I., Miyazakı,A., Sakai,K., Sasakı,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

e.S., Rogers,J., Birney,E. and Hayashizaki,Y.

of 60,770 full-length cuthas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepare mouse tissues.

Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Cmaha,NB 66131 USA) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 GGGGGGGGCGCAGTGCCGGGGTCCTTCTCGACCCGCAGCCACCACCACCGCCGGCGGTGA 126
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Pred. No. 2.2e-24;
0; Mismatches 1; Indels 0;
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/clone="F930042F15"
                                                                                                                                                                                                                                              Contact: Yeshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /moi_type="mRNA"
/strain="C57BL/60"
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bD0.a02.gl Canis cowas from testes cells Canis familiaris otwa
clone hb0la02 5', mRNA sequence.
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TICTTGIGITHACTGIAAGAAAGITAAGICAATCAACCCCGGCAAGCTCAGGGGTGIGT 1012
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                                                                                                                          ATGTCTTAATTCCAAACCGGATGAGTGGTGAGTGCCAGTCTCCAGACTGCCCTGGAACCA, 738
                                                                                                                                                                                                               739 GAGCIGAATITTTGTTTAAATGTGGAGCACACGGAACCICAGACAAGGACAAGGGACA
                                                                                                                                                                                                                                          771 GGGAGCTGGTCCTGGTATTCCAGTGTGCAGAGTCATGTGARTCTGTGTGTCACGTTTCC 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  919 ACTTGTATTGTGTGACAAAGACTCAAGGATGGGCAGTTTGTCCACGATGCTCAACTTGGCT 978
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                                                                  1011 TGCAGCASCTGCASAGAACAACATTCCACCTTCAGCAGGGGGTCGTCGTGGTGGGGGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1336 AGGAGGCCTCCAAGGAAACCATCAAGAAGAACCAAGGCTTGTCCTCGCTGCAAGGTGC
                                                                                                                                                                     951 AIGICITICOICCCAGGICGIGITCACGGITTOIGICAATCAGACGCTIGIGIGIGGGGAACG
                                                                                                                                                                                                                                                                                               CTITIGAACCTGATCACCAGCAACAGGGGCAGCATCCCTTGCATAGCGTGGACAGATGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTGGCACCTGCAAACAAGCAACCCTC--ACCTTGGCCCAGGGCCCATCTTGCTGGGACG
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//issue_type="heads and internal organs combined"
//des_tage="heads and internal organs combined"
//des_tage="adult"
//done_lib="SHGC-CDA"
//cone_lib="SHGC-CDA"
//cone_adptor; Site_2: Xhoi (3, linker primer); The mixed organ cDA library was generated using the ZAP-CDNA method organ cDA library was generated using the ZAP-CDNA method organ cDA library primer containing an oligo dT sequence preceded by a synthetic Xhoi site. 5 prime adaptors were used containing an ECORI cohesive end. The finished cDNAs were inserted in to the ZAP express vector with respect to the lacZ promoter of pBK-CNV. An amplified library was prepared from approximately allilion primary closes in the lambda ZAP Express vector. In vivo excision was then used to generate individual pBK-CNV phagemid clones for
                                                                                                                                                                                                                                   CD498236 LI42 bp mRNA linear EST 12-JUN-2003
CD432-D10.yld-s SHGC-CDA Gasterosteus aculeatus cDNA cione
CD432-D10 3', mRNA sequence.
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Kingsley, D.M., Peichel, C., Ralabahdra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.

Expressed sequence tags from Gasterosteus aculeatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITITCATCTACTGCAAAGGCCCCCTGCCACAAGGTCCAGCCTGGAAAGCTGCGAGTTCAG 620
                    CTGATCACCACCACAACAG-GCGCAGCATCCCTTSCATAGCGTGCA-AGATGTCAGGAGCC 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
Contact: Kingsley, DM
HHMI and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B100, 279 Campus Drive, Stanford, CA 94305-5329,
Tel: 650, 725 5954
Fax: 650 725 7739
Email: kingsley@cmgm.stanford.edu
                                                          301 CTGATCACCANCANCAGCCCGCAGCATCCCCTGCATCGCGTGCACGGGATGTCAGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.3%; Score 302; DB 14; Length 1142; 60.2%; Pred. No. 2.5e-20; atlive 0; Mismatches 365; Indels 17
                                                                                                    CTGTCCTGGTCTTCCAGTGTAACCACCGTCACCGTGATCTTTG 908
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Gasterosteus aculeatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/Arsin="Salinas river, CA"
/db xref="taxon:69293"
/clone="CDA32-D10"
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High quality sequence start: 14
High quality sequence stop: 654.
Location/Qualifiers
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326 c 27
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CD498236.1 GI:31425267
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CRIGIN
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Canis familiaris (dog) Canis familiaris

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238

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A1228346 SOCT-1998 SST225041 Normalized rat brain, Bento Soares Rottus sp. cDNA clone RBRCT55 3' end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3162 TACCTGAAGICIGTGTGTGTGGTGGTACCCAGACTGTCAATCAATAAAGACCCAGACTGT 3221
                                                                                                                                                                                                                                                                             Rattus sp.
Rattus sp.
Bukaryota: Metazoa: Chordata: Cramata: Vertebrata: Buteleostomi;
Mammalia: Butheria: Rodentia: Sciurognathi; Muridae: Murmae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REST) Catalog & Rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              397 csrákrssckrsssskarsckksakákristristratritatritisszrakásáketek
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Glodek,A. Ghandra,I., Mason,T.M., Quackenbush.C.
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog
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/db_xref=taxon:10:18"
/clone="RBRCTS"
/clone="Brormalized rat brain, Bento Soares"
/note="Organ: brain; Vector: pT773Pac: Site_1: 8
Site_2: Not1" 77 g 122 t
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al Similarity 85.8%; Pred. No. 4.56-18;
338; Conservative C: Mismatches 51; Indels
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  SZ6 CAGCCAGAGGTCCAGTTAAACGCACCTAGAGAGAGG 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Lee, NH
The Institute for Genomic Research
9712. Medical Center Drive, Rockville,
Tel: (301)-838-3529
Fax: (301)-838-029
Emal: chiee%tgr.org
                         /organism="Rattus sp
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A1228346.1 GI:3812233
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ORGANISM
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AI228346/C
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/clone_lib="Canis cDNAs from testes ceils"
/clone_lib="Canis cDNAs from testes ceils"
/note="Vector: Lambda Zap II, The library was produced by Greg Hamon and Raymond Preston (Cold Spring Harbor Laboratory). This library is cligo(dT) primed using stratagene zap cDNA synthesis kit. It was made from dog trestes. Please contact Greg Hamon (hamon@cshl.org) with any library relacd inquiries."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                         1 (bases 1 to 519)
O'Shaughnessy, A.L., McComb.e, W.R., Baker, J.P., Balija, V., Cunnius
O'Shaughnessy, A.L., McComb.e, W.R., Baker, J.P., Balija, V., Cunnius
O'D., Dedhia, N.N., de la Bastide, M., Katzenberger, P., King, L.,
Kirchoff, K.A., Miller, B., Muller, S., Nascimento, L.J., Palmer, J.,
Santos, J., Shah, R.S., Spiegel, L.A., Zutavern, T., Preston, R. and
Hannon, G.J.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 CAGCCTCCACCTGCCTAGTGACCATGATAGTGTTCGTCAGGTTCAACTCCAGCATGGTT
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                  Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
1 (bases 1 to 519)
                                                                                                                                                                         Expressed sequence tags from Canis familiaris (dog) (2002)
Unpublished
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9.0$; Score 291.8; DB 12; Length
Best Local Similarity 74.2$; Pred. No. 4.6e-19;
Matches 382; Conservative 3; Mismatches 132; Indels
                                                                                                                                                                                                           Contact: W. Richard McCombie
Lita Annerberg Hazen Genome Sequencing Center
Cold Spring Hazbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8884
Hajf grain mccombie@cshl.org
Seq primer: -21M13UnivRev
High guality sequence stop: 519.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Canis familiaris"
/mol type="mRNA"
/db xref="taxon:9615"
/clone="hb0la02"
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2982

27.8

3042

2:8

3261

5.5

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/organism="Mus musculus"
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UI-X-BH2.3-aoc-f-08-0-UI.rl NIH BMAP_M_S3.3 Mus musculus cDMA clone UI-X-BH2.3-aoc-f-08-0-UI.r, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: M.S. Scares Lab Clone distribution:

CDNA Library Preparation: M.S. Scares Lab Clone distribution:

Should be noted that Bento Scares is generating a small number of
additional specialized non-redundant arrays of BMAP CDNAs wnose
availability will be considered under appropriate and limited
collaborative arrangements
Seq primer: M.S. Reverse
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                 Mis musculus (house mouse)
Mus musculus
Bikaryota, Metazoa, Chordata, Craniata, Vertebrata, Bureleostomi,
Mammalia, Eutheria, Rodentia; Sclurognathi; Muridae; Murinae; Mus
1 (bases 1 to 274)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Chin, H
National Institute of Mental Health
Cost Securive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Par: 101 443 1766
Par: 101 443 9830
Email: ESTPerail.nih gov
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   3229 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3255
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97044477
                                                            34 TAAGTACCCAGACTGTCAATAAAAAA 8
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                BF286222
EST450813 Rat Gene Index, normalized rat, Rattus norvegicus CDNA
Rattus norvegicus CDNA clone RGIFN37 3' sequence, mRNA sequence.
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/lab host="DHS-alpha"
/clone lib="Rat Gene Index, normalized rat, Rattus
norvegicus cDNA"
/note="Vector: pT3T7Pac, Site_1: Ecos1, Site_2: Not1,
Combination of ROV, RBR, RXI, RLI, RPL, RLU, REM, RWU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
Contact: Lee, NH
Contact: Lee, NH
First include Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-1529
Email: nhlee@tirorg
This clone is available through the ATCC, contact the ATCC
tel#103-355-2700 for further information.
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/mo._type="mRNA"
/db_xref="taxon:10116"
/cicne="RGIFN37"
41 CAATCAATAAGTACCCAGACTGTCAATAAAGAA
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Query Match
8.4%; Score 272.4; DB 10; Length 274;
Best Local Similarity 99.6%; Pred. No. 5.5e-17;
Matches 273; Conservative 0; Mismatches 1; Indels 0; Gaps
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Search completed: October 24, 2003, 13:32:05 Cob time : 4330 secs

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| SIDSI/gcgdata/geneseqfy.embl/AA1999.DAT: |
| SIDSI/gcgdata/geneseqfy.embl/AA1990.DAT: |
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2570
I MIVFVRFNSSYGFPVEVDSD......CWNCGCEWNRACMGDHWFDV 464
                                                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Query Match Length DB	464	464	464	48.	465	465	465	437	344
	Query Match	100.0	8.66	99.8	9.96	84.5	84.5	84.5	77.6	72.6
	Score	2570	2565	2565	2483	2171.5	2170.5	2170.5	1993.5	1867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243
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                                                                                      The present sequence represents a murine parkin2 polypeptide. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region 6q25.27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Hutington's disease, amyotrophic lateral sclerosis, Multi-system arrophy, Milson's disease, Prion disease, and secondary causes inducing Pick's disease. Frion disease, and secondary causes inducing Parkinson's syndromes like toxins, draugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin protein.
                                                                                                                                                                                                                                                                                                                                                                    I MIVEVRENSSYGEPVEVDSDISILOLKEVVAKROGVPADOLRVIFAGKELPNHITVONCD
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                                                                                                                                                                                                                                                                                           100.0%; Score 2570; DE 22; Length 464; 100.0%; Pred. No. 2.6e-236;
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            New polynucleotides encoding mouse parkin2 protein, useful
producing a transgenic non-human animal as an animal model
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                                                                Disclosure; Page 17-19; 62pp; English.
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The present sequence represents a murine parking polypeptide. The sequence contains the mutation lysiblash. Mutations or delections in the parking dene cause Parkinson's disease in humans. The human parking gene is located in gene region 6025.2-27. Parking polypeptides and polymicleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkingon's disease, Allaheimer's disease, Huntington's disease, amyotrophic lateral solerosis. Multi-system arrophy, Wison's disease, Prox disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma travely, associated with a less active or non-active parkin
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                                                                                                                                                                                                                                                                                                                                        New polynucleotides encoding mouse parkin2 protein, useful producing a transgenic non-human animal as an animai model neurodegenerative diseases
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99.6%; Pred. No. 7.8e-236;
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                                                                                                                        HENDY - PROPERTY GREEK GMEH
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99EP-0116766
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N-PSDB; AAF55258.
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Alzhermer's disease, Huntington's disease, amyorxophic laveral sclerosis,
Aulti-system atrophy, Wilson's disease, Pick's disease, Prion disease,
brain tumour, head trauma, stroke, vascular irregularity,
                                                                 CWDDVLIPNRMSGECQSPDCPGTRAEFFFKCGAHPTSDKDTSVALNLITSNRRSIPCIAC 240
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                                                                                                                                                                                                                                                                           231 HHFRILGESQYTRYQQYGASECVLQMGGVLCPRPCCGAGJJPEQGQRKVTCEGGNGJGCG 360
                                                                                                                                                                                                                                                                                                                          FVPCRDCKEAYHEGDCDSLLEPSGATSQAYRVCKRAAEQARMEEASKETIKKTTKPDPRC 420
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TDVRSPVLVFQCNERHVICLCCFHLYCVTRLNGRQFVHDAQLGYSLPCVAGGPNSLIKEL
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ucing a transgenio non-human animal as an animal model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
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neurodegenerative diseases
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                                                                                                                                                                                                                                                                                                                      Parkin2: Parkinson's disease, 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huttington's disease; amyotxophic lateral sclerosis; Multi-system atrophy; Milson's disease; Pick's disease; Prion disease; brain turour; Read trauma; Stroke; Vascular irregularity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a murine parkin2 polypeptide. The sequence contains the mutation Thr415Aen. Mitations or delections in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polymucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as parkinson's disease. Altheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, and secondary causes inducing fastinson's system attophy, Milson's disease, Pick's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin
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Pred. No. 7.8e-236;
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463; Conserv
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WFI; 2003-046812/04.
N-PSDE; AAD47680.
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Best Local Similarity
Matches 388; Conserv
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  brain tumours, head trauma, stroke, vascular irregularities or memabolic
irregularities, associated with a less active or non-active parkin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 HHFRILGEBOYTRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEQGQRKVTCEGGNGLGCG
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                                                                                                                                                            Gaps
                                                                                                                 96.6%; Score 2483; DB 22; Length 451;
.larity 100.0%; Pred. No. 5e-228;
Conservative 0; Mismatches 0; Indels 0
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126
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                                                                                                                                   Local Similarity es 451; Conserv
                                                                              451 AA;
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Synthetic.
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                                                                              Sequence
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                                                                                                                   Query Match
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Matches
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The invention relates to Farkin protein and its corresponding nucleic acid sequence. The mucleic acid sequence is useful for altering the proteocytic processing of Parkin at the pretential cleavage site at Asp. 126. The invention is used in manufacturing or testing a plantaceutical composition for treating and/or preventing a neurological discrete, e.g. Althermet's disease or isohaemic stroke. It also used for detecting the cocurrence of proteolytic processing of Parkin at Asp. 126 in a sample, in monitoring a pocential disposition for a neurodegenerative disease, and for treating, preventing and/or diagnosing Parkinson's disease or other neurodegenerative disorders. The viral vector is used for transforming neuronal cells in vivo or ex vivo. The invention is useful for neurotransplantation into the CMS of a mammal it may be used in screening assays to identify compounds that increase or decrease approprise it is also used in gene therapy. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MIVEVRENSSYGEPVEVDSDTSILQIKEVVAKROGVPADQLRVIFAGKELPNHLTVQNCD
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llarity 83.4%; Pred. No. 2.8e-198;
Conservative 30; Mismatches 46; Indels
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29-MAR-2001, 2001DK-0000525.
03-APR-2001, 2001US-281286F.
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The invention relates to Parkin protein and its corresponding nucleic acid sequence. The nucleic acid sequence is useful for altering the proteolytic processing of sequence is useful for altering the proteolytic processing of manufacturing or testing a pharmaceutical composition for treating and/or preventing a neurological disorder, e.g. Alzheimer's disease or ischaemic stroke. It also used for detecting the occurrence of proteolytic processing of Parkin at Asp 126 in a sample, in monitoring a potential disposition for a neurodegenerative disease, and for treating, preventing and/or disposing Parkinson's disease or other neurodegenerative disorders. The viral vector is used for transforming neuronal cells in vivo or ex vivo. The invention is useful for neurotransplantation into the ONS of a nammal T may be used in screening assays to identify compounds that increase or decrease
361 GFAFCRECKEAYHEGECSAVFEASGTTTGAYRVDERAAEQARWEAASKFTIKKTTKPCPR 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, Parkin protein, neurological disorder, apopiosis, gene therapy, ischaemic stroke, Parkinson's disease, Alzheimer's disease, noctropio, transgenio, cerebroprofective, neuroprofective, neuroprofective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid sequence encoding a Parkin polypephide, useful for treating, preventing or diagnosing neurological disorders, e.g. Parkinson's disease, Alzheimer's disease or ischemic stroke, and in screening assays
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                            CNVPIEKNGGCMHMKCPQPQCKLEWCWNCGCEWNRACMGDHWFDV 464
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Best Local Similarity 82.4%, Pred. Mo. 3.56-198;
Matches 788; Conservative 23; Mismatches 47; Indels
                                             CHYPVEKNGGCMHMKCFQPQCRLEWCWNCGCEMNRVCMGDHMFDV
                                                                                                                                                                                                                                                                                                                                                             Docation/Qualifiers
126
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                                                                                                                                         AAE30800 standard; Protein; 465
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03-AFR-2001; 2001US-281286P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is encoded by a gene of the invention, and is implicated in the pathology of Parkinson's disease. This sequence is a variant of the parking gene found in parkinson's disease patients. The sequences may be used for the diagnosis, treatment (including gene therapy) and investigation of Parkinson's disease.
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                                                                                                                                                        Parkinson's disease related gene; parkin gene; variant; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.5%; Score 2170.5; DB 20
83.4%; Pred. No. 3.5e-198;
live 29; Mismatches 47;
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                            Z
                                                                                                                        Human parkin gene variant protein.
                           AAY32501 standard; Protein; 465
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Best Local Similarity 83.4
Matches 388; Conservative
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(SHIM/) SHIMIZU N.
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Parkin2, Parkinson's disease, 6q25.2-27, neurodegenerative disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral solerosis; Multi-system arrophy, Milson's disease, Pick's disease, Prion disease, brain tumour, Read traimal stroke, vasoular irregularity.
                                                                                                                                                                                                                                                                                                CIDVRSPVLVFQCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLPCVAGCPNSLIKE
                                                                                                                                                                                                                                                                                                                                                                                                            MIVEVRPNSSYGFPVEVDSDTSILQLKEVVAKRQGVPADQLRVIFAGKELPNHLTVQNCD
                                                                                                     LEQOSIVHIVORPRARSHETNASGGDEPÇSTSEGSIMESRSLTRVDLSSHTLPVDSVGLA
                                                                                                                                                                           41 LDÇQSIVHIVQRPWRKGÇEMNATGGDDFRNAAGGCEREPQSLTRVDLSSSVLPGDSVGLA
                                                                                                                                                                                                             121 VILDIDSKADSBAARGPV-KPTYNSFIYCKGPCHKVQPGKLRVQCGTCKQATTILAQGP
                                                                                                                                                                                                                                  180 SCWDDVLIPNRMSGECQSPDCPGTRAEFFFKCGAHPTSDKDTSVALNLITSNRRSIPCIA
                                                                                                                                                                                                                                                                                                                                            CTDVRSPVLVFQCNHRHVICLDCFHLYCVTRLMDRQFVHDAQLGYSLPCVAGCPNSLIKE
                                                                                                                                                                                                                                                                                                                                                                                                                             360 GEVECROCKEAYHEGDCOSULEPSGATSQAYRVOKRAAEQARWEEASKETTKKTTKPCPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 GPAFCRECKEAYHEGECSAVFEASGTITQAYRVDERAAEQARWEAASKETIKKTIKPCPR
                                                   Gaps
                                                   99
                 Length 437,
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for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNVPIEKNGGOMHYKOPQPQCKLEWCWCGCEWNRACMGDHWFDV 464
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHYPVERNGGCYHMKCPOPQCRIEWCWNGGCEWNRYCMGDHWFDV
                  DB 20;
                                                   ,5;
                  Score 1993.5; DB ;
Pred, No. 2.5e-191
                                                 Mismatches
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                                                   29;
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                  77.6%;
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                                                 362; Conservative
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N-PSDB; AAF55248.
                                    Similarity
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                 Query Match
Best Local S
Matches 362
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                                                                                                                                                                                                                                                                                            LHHFRILGEEQYTRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEQGQRKVTCEGGNGLGC
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                                LEÇÇSIVHIVÇRPRRRSHETNASGGDEPQSTSEGSIWESRSLTRVDLSSHTLPVDSVGLA
                                                             61 LOQQSIVHIVQRPWRKGQEMNATGGDDPRNAAGGCEREPQSLTRVDLSSSVLPGDSVGLA
                                                                                              VILDTDSKRDSEAARGPV-KPTYNSFFIYCKGPCHKVQPGKLRVQCGTCKGATLTLAQGP
                                                                                                                             121 VILHTUSRKDSPPAGSPAGRSIYNSFYVYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGP
                                                                                                                                                                                                                              CTDVRSPVLVFQCNHRHVICLDCFHLYCVTRLNDRQFVHDAQLGYSLPCVAGCPNSLIKE
                                                                                                                                                                                                                                                                                                                  1 MIVEVRENSSHGFPVEVDSDTSIFQLKEVVAKRQGVPADQLRVIFAGKELRNDWTVCNCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkinson's disease related gene; parkin gene; variant; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene implicated in the pathology of Parkinson's disease, treatment of the disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   investigation of Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 89-94; li4pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human parkin gene variant protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-494295/41.
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Amino acid sequence of a murine parking polypeptide
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Best Local Similarity
Matches 289; Conserv
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                            EP1081225-A1
                                                                                    30-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 FVFCROCKEAYHEGOCDSLLEPSGATSQAYRVDKRAAEQARWEEASKETIKKTTKPCPRC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkin2, Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzhadhar's disease, Huntington's disease; amyotrophic lateral solerosis; Multi-System atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VILDTDSKRDSEAARGPVKPTYNSFFIYCKGPCHKVQPGKLRVQCGTCKQATLTJAQGPS 180
                                                                                                                                                                                                                                                                                                                                            1 MIVEVRENSSYGEPVEVDSDISILQLKEVVAKRQGVPADQLRVIFAGKELPNHLIVQNCD 60
                                                                                                                                                                                                                                                                                                                                                                 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotide sequence contains a deletion, leading to a truncated bycotein. Mutations or deletions in the parking gene cause parkinson's disease in humans or human parking gene is located in gene region 6425.2-27. Parkins polypeptides and polynucleotides are useful for analysing neurodegenerative disease. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-system atrophy, Wilson's disease, pick's disease, prion disease, and secondary causes inducing parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular integularities or metabolic irregularities, associated with a less active or non-active parkin protein.
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                                                                                                                                                                                                                                                                                                                     Gaps
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                                                        The present sequence represents a murine parking polypeptide.
                                                                                                                                                                                                                                                                                     72.6%; Score 1867; DB 22; Length 344;
Larity 74.1%; Pred. No. 2.1e-169; No. 2.1e-169; Conservative 0, Mismacches 0, Indels 120
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                           Claim 7; Page 40-41; 62pp; English
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neurodegenerative diseases
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Matches 344; Conserv
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CWDDVLIPNRMSGECQSPDCPGTRAEFFKCGAMPTSDKDTSVALMLITSMRSIPCIAC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a muxine parking polypoptide. The polypholeocide sequence contains a deletion, leading to a truncated discussion. Mutations or deletions in the parking gene cause Parkinson's disease in humans. The human parking gene is located in gene region 6Q5.2-27. Parking polyphoptides and polynocleotides are useful for analysing neurodegenerative diseases. They are also useful for resting the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzielment of a neurodegenerative disease such as Parkinson's disease, Anzielment of a neurodegenerative disease, amyotrophic lateral sclerosis, Multi-system atrophy, Mison's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain function, head trauma, stroke, vascular intregularilies or metabolin irregularilies, associated with a less active or non-active parkin protein.
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al Similarity 100.0%; Pred. No. 3.1e-139;
289; Conservativo 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                          New polynucleotides encoding mouse parking protein, useful producing a transgenic non-himan animal as an animal model
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(BICF-) BIOFRONTERA PHARM GMBH
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Parkinz, Parkinson's disease, 6q25.2-27, neurodegenerative disease,
Alzhermer's diseases, Huntington's disease, anyotrophic lateral sclerosis,
Multi-system arrophy, Wilson's disease, Prok's disease, Prion disease;
brain tumour, head trauma, stroke, vascular litegularity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCWDDVLIPNRMSGECQSPDCPGTRAEFFFKCGAHPTSDKDTSVALNLITSNRRSIPCIA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a murine parking polypeptide. Mutations or deletions in the parking gene cause Parkinson's disease in himmans. The human parking gene is located in gene region 6q25.2-27. Parking polypeptides and polymudicolides are useful for analysing nourodegenerative diseases. They are also useful for testing the efficacy of the treatment of a nourodegenerative disease, and secondary disease, Huntington's disease, Parkinson's disease, Huntington's disease, Parkinson's disease, Multi-system atrophy, Mison's disease, Prion disease, and secondary causey inducing Parkinson's syndromes like toxinis, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MIVEVREMSSYGEPVEVDSDISILDIKEVVAKRQGVPADQLRVIFAGKEIPNHLIVQNCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 LEQQSIVHIVÇRPRRRSHETNASGGDEPQSTSEGSIWESRSLTRVDLSSHTLPVDSVGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MIVEVRENSSYGEPVEVDSDTSILQEKEVVAKRÇGVPADQLRVIFAGKELPNHLIVÇNCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VILDTOSKROSEAARGP-VKPTYNSPFIYCKGPCHKVQPGKLRVQCGTCKQATLTLAQGP
                                                                                                         sequence of a murine parkin2 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.7%; Score 1276.5; DE 2
99.6%; Pred. No. 3.4e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides encoding mouse parking producing a transgenic non-human animal as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Fage 19-20; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BICF-) SIOFRONTERA PHARM GMBH
                                                                                                                                                                                                                                                                                                                                                                                                          99EP-0116766.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurodegenerative diseases
                                                             (first entry)
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Best Local Similarity 99.6
Matches 243; Conservative
                                                                                                                                                                                                                                     metabolic irregularity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-212797/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                          30-AUG-1999;
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                                                           29-MAY-2001
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                    AAB67518;
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                  Parking: Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; myotrophic lateral sclerosis; Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEQOSIVHIVORPRRISHETNASGGDEPQSTSEGSIWESRSLTRVDLSSHTLPVDSVGLA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LEQQSIVHIVQRERRREHETUASGGBEDQSTSEGSIWESRSLIRVDLSSHTLPVDSV51A 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCWDDVLIPNRMSGECQSPDCPGTRAEFFRCGAHPTSDKDTSVALNLITSNRRSIPCIA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a murine parkin2 polypeptide. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene cause Parkinson's disease in humans, polypeptides and polymorleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-system arrophy. Wilson's disease, Prior disease, may secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head traims. Stroke, yascular irregularities or metabolic irregularities, associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 VILDTDSKRDSEAARGP-VKPTYNSFFIYCKGPCHKVQPGKLRVQCGTCKQATTTLAOGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MIVEVRENSSYGEPVEVDSDISILOLKEVVAKROGVPADQLRVIFAGKELPNHLIVQNCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides encoding mouse parking protein, useful producing a transgenic non-human animal as an animal model neurodegenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.9%; Score 1281.5; DB 23
99.6%; Pred. No. 1.1e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with a less active or non-active parkin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                Parkin2; Parkinson's disease; 6q25.2-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Page 21-22; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                              (BIOF-) BICFRONTERA PHARM GMBH
                                                                                                                                                                                                                                                                         99EP-0116766
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Best Local Similarity 99.6
Matches 244, Conservative
                                                                                                    metabolic irregularity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAF55246
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                                                                                                                                                                                                                                                                                                                                                                                                       Luebbert H;
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procein, useful an animal model

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CTDV 243

240

RESULT :2 AAB67518 ID AAB67518 standard, Protein, 262 AA.

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Gaps ;

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DB 22; Length 262

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238 CVAGCPNSLIKELHHFRILGEEQYTRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEQGQR 347
                                                                                                                                                                                                     348 KVICEGGNGJGGGFVECRDCKEAYHEGDCDSULEPSGAIT---SGAYRVEKRAABQARWEE 404
                                                                                                                                                                                                                                       Alzheimer's disease, Hunrington's disease, amyotrophic lateral solerosis,
Muiti-system atrophy, Milson's disease, Pick's disease, Prion disease,
braim tumour, head trauma, stroke, vascular irregularity,
                                                            IKNNIKAVPCLACIDVSDIVLVFPCASQHVICIDCPRHYCRSRLGERQFYPHPDFGYTLP 295
                     228 ITSNRRSIFCIACTDVRSPVLVFQCNHRHVICLDCFHLYCVTRLNDRQFVHDAQLGYSLP 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a murine parking polypeptide. The polypucleotide sequence contains a deletion, leading to a truncated disease. Mutations or deletions in the parking gene cause Parkinson's disease in humans. The human parking gene is located in gene region 6425.2-27. Parking polypeptides and polypucleotides are useful for analysing neutrodegenerative disease. They are also useful for testing the efficiency of the treatment of a neutrodegenerative disease such as Parkinson's disease. Altherment of a neutrodegenerative disease such as advortoble lateral solections. Will: System althophy, Wison's disease, pron disease, and secondary causes indusing parkinson's syndromes like toxins, drugs, brain timours, head trauma, stroke, vascular infigularities or metabolic irregulatities, associated
                                                                                                                                                                                                                                                                                                  405 ASKETIKKTTKPCPRONVFIBKNGGGMEMKGPQPQCKLBWCWNGGGBWNRAGMGDHWF 462
                                                                                                                                                                                                                                                                                                                               296 CPAGCERSPIBETHNEKLLTREBYDRYÇRFATEEYVIQAGGVICPÇPGCGMGLLVEPDOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkin2: Parkinson's disease; 6q25.2-27; neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a murine truncated parkin? polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynuclectides encoding mouse parkin2 protein, useful i
producing a transgenic non-human animal as an animal model ;
meurodegenerative diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR67525 standard: Protein; 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPI 081225-A1
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                                                                 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 ELQLESEERLNITDEERVRAKA-----HFFVHC-SQCDKLCNGKJRVRCALCKGGAFTVH 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VEVRENSSYGEPVEVDSDISILQLKEVVAKROGVPADQLRVIFAGKELPNHLIVQNCDLE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-bell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPC at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 IVVKINTGKTLIVNLEPQWDIKNVKBLVAPQJGLQPDDLKIIFAGKELSDATTIEQCDLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 QQSIVHIVQ-RP--RRRSHETNASGGDEPQSTSEGSIWESRSIJRVDLSSHTLPVDSVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 AVILDIDSK---RDSEAARGPVKPTYNSFFIYCKGPCHKVQPGKLRVQCGTCKQATLTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 QGPSCWDDVLIPNRMSGECGSPD--CPGTR-----ABFFFKCGAHPT-SDXDTSVALNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 46; Gaps
                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 22134; 21pp + Seguence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dength 468;
                                                                                                                                                                                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 22134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.9%; Score 1078; DB 22;
43.7%; Pred. No. 6.7e-94;
tive 78; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wyers
                                                                                                           ABB65114 standard; Protein; 468 AA.
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Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M.
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CTDV 244
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                                                                                                                                                       AB365114;
241
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                                                                                                                                                   61 LEQUESTVHIVORPRREHEINASGEDEPOSTSEGSIWESRSLIRVDLSSHTLPVDSVSTA 120
                                                                                                                                                                         61 JEQQSIVHIVQRPRRRSHETNASGGDEPQSTSEGSIWESRSLTRVDLSSHTLDVDSVSLA 120
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                                                                            1 MIVFVRFNSSYGFPVEVDSDTSILQLKEVVAKRQGVPADQLRVIFAGKELPNHLTVQNCD 60
                                                                                                        1 MIVEVRENSSYGFPVEVDSDTSILQLKEVVAKRQGVPADQLRVIFAGKELPNELTVQNCD 60
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   Length 183,
                                         Indels
Query Match
35.7%; Score 917; DB 22;
Best Local Similarity 100.0%; Pred. No. 4.2e-79;
Matches 177; Conservative 0; Mismatches 0;
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35.7%; Score 917; DB 22; Length 194;

Query Match

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         al Similarity 100.0%; Pred. No. 4.6e-79; 177; Conservative 0; Mismatches 0;
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Patent No. Sequence

Sequence 94, Appl Sequence 94, Appl Sequence 100, Appl Sequence 100, Appl Sequence 24, Appl Sequence 2, Appl

us-09-830-703-4.rai

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208 FPKCGAHPTSDKDTSVALNJITSNRRSIPCIACTDVRSP--VLVFQCNHRHVICLDCFHL
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Sequence 13, Application US/09914259
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Parent No. 849539
Parent No. 8471-010-999
Parent Parent No. 87471-010-999
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Best Local Similarity 28.8%; Pred. No. 1.46-18;
Marches 79; Conservative 37; Mismatches 97;
                      US. 08-505-486-94
US. 08-801-028-94
US. 09-482-6118-94
US. 09-482-6118-100
US. 09-482-6118-100
US. 09-482-6118-100
PCT-US95-0918-100
PCT-US95-0918-100
US. 08-462-625-094
US. 08-462-694
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US-09-198-006A-2
Sequence 2. Application US/08298006A
) Parent No. 5665588
) GENERAL INFORMATION:
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(c) 1993 - 2003 Compugen Ltd.
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US-08-198-109A-2
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US-08-934-306-41
US-08-934-306-41
US-08-93-48-611B-99
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Perfect score:
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                                                                                                                                                         protein -
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Gaps

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207 PAPDOGYAVIAYGOASOP----KLTCERE-- GOGTEFÖYHOKQIWHPKQTGDMARQ-- 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 PRPGCGAGLL-----PECGQRKVTCEGGNGLGCGFVFCRDCKEAYHEGD-CDSLLEPS 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 GATSQAYRV-DKRAAEQARWEEASKETIKKTTKPCPRCNVPIBK--NGGOMHMKCPQPQC-440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 QFVHDAQLGYSLPCVAGCPNSLIKELHHF**-RILGEBQYTRYQQYGAEECVLQMGGVLC 331
                             GENERAL INFORMATION:
APPLICANT: MORDAUT. Jack:
APPLICANT: MORDAUT. Jack:
APPLICANT: MORDAUT. Jack:
APPLICANT: MORDAUT. Jack:
FILE REPRENCE: D3705CIP/UB
CURRENT APPLICATION NUMBER: US/08/893,333A
CURRENT FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 ACCPP-----PEALPAE-----PAASAEAAAGAEPGFDDESAASGG--GPGGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.2%; Score 186; DB 2; Length 587;
25.5%; Pred. No. 1.4e-10;
tive 28; Mismatches 104; Indels 116;
                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Amino acid sequence of Natural Killer Lytic OTHER INPORMATION: Associated Process encoded by mucheotides OTHER INPORMATION: 190 to 1953 of Sequence ID. No. 5591705 1 atent No. 5981705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 ---HDIRLILADP-----PLMHKYEEFIVRRYLASDPDCRW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Innes, Michael
APPLICANT: Creasey, Abla
ITLE OF INVENTION: Production of Tissue Factor Pathway
TITLE OF INVENTION: Inhibitor
NUMBER OF SEQUENCES:
ADDRESSMEN ADDRESSE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUX TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.30B
CUSREMT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 IPCIAC----TDVRSPVIVFQCNHRHVICLDCFHLY----
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    Sequence 2, Application US/08893335A
Patent No. 5981705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09854764 Patent No. 6103500 GENERAL UNFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chiron Corp.
eff: 4560 Horton St.
Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 25.5'
Matches 85; Conservative
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                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Homo sapiens
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CITY: Em
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.2%; Score 186; DB 1; Length 587; Best Local Similarity 25.5%; Pred. No. 1.4e-10; Matches 85; Conservative 28; Mismatches 104; Indels 116; Gaps
APPLICANT: Kormbluth, Jacki
TITLE OF INVENTION: DNA Encoding Natural Killer Lytic Associated
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage COMPUTER: MACINTOSH IIC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 GCEFCWLCMKEISDLHYLSPSGCTFWGKKPWSR 342
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CORPUTER: MACINTOSH IIC:
CORPUTER: MACINTOSH IIC:
CORPUTER: Microsoft word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/03/398,0C8A
FILING DATE: March 2, 1995
CLASSIFICATION: 435
FRICA APPLICATION NUMBER: 08/126,531
FILING DATE: 24.5EP-193
ATTORNEY/AGENT INFORMATION:
NAME: Adier, Dr. Berjamin Aarch
REJESTRATION NUMBER: 35,423
REJERENCE/DOCKET NUMBER: D5705CIP
TELECOMMUNICATION INFORMATION:
METERENCE/DOCKET NUMBER: D5705CIP
                                                                                                                  E: Gilbreth & Adler, P.C.
8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (713) 777-2321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FCR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPCLOGY: linear
MOLECULE TYPE: Protein
HYPOTHETICAL: No
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STRANDEDNESS:
                                                                                                                                                                   Houston
                                                                                                                                                                                                               USA
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                                                                                                                                                                                    STATE: T
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RESULT 3 US-08-893-333-2

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61 LEQQSIVHIVQRPRRSHETNA-------SGGDEPOSTSEGSIWESRSLT 103
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                                                                                                                                                                                                                                     61 LEQOSIVHIVORPRRSHETNASGGDEPOSTSEGSIMESRSLTRVDLSSHTLPVDSVGLA 120
                                                                                                                                                                                          I MOJEVKILIGKTITLEVESSDIJONYKSKIODKEGIPPDQQRLIFAGKQLEDGRTLSDYN 60
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5.2%, Score 134, DB 1, Length 1121,

Bost Local Similarity 24.8%, Pred. No. 0.0001,

Matches 38, Conservative 38, Mismatches 47, Indels 30, Gaps
                                                                                                                                                                                                                                                                                                                                                       121 VILDID-----SKRDSERARGPVKPTYNSF------FIY--CKG 151
                                                                                                          993
                                                             Query Match

5.3%, Score 136, DB 5, Length 552,
Best Local Similarity 25.6%, Pred. No. 1.1e-35,
Matches 44, Conservative 28, Mismatches 44, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Hamilton, Brock, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMPLEAURY 1, 100 S212058
GENERAL INFORMATION:
APPLICANT: Baker, Rehan 7,
APPLICANT: Tobias, John 4,
APPLICANT: Varshavsky, Alexander
ITILE OF INVENTION: Ubiquitin-Specific Picteases
NUMBER OF SQUENCES: 8
CORRESPONDENCE ADDRESS: 8
CORRESPONDENCE ADDRESS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.3, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                              61 IQKESTLHIVIRIA-----GGDSEED----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-5091AA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/07/789,915A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPTTER EGADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS
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617-861-9540
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CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19911108
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/ MCLECULE TYPE: protein
PCT-US95-09377-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
FILING DATE: 199111(
CLASSIFICATION: 435
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US-07-789-915A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      # MIVFVRFNSSYGFPVEVDSDTSILQLKEVVAKRQGVPADQLRVIFAGKELPNHLTVQNCD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---- EEHT---- 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 VILDID-----FIY--GKRDSEAARGPVKPTYNSF------FIY--CKG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                5.3%; Score 136; DB 3; Length 352;
25.6%; Pred. No. 1.1e-05;
tive 28; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application PC/TUS9509377
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FIGURE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTEN RElease #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09377
FILING DATE: 25-JULY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 IQKESTLHLVLRLR-----GGDSEED---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/COCKET NUMBER: 0991.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286,530
FILLING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
                                                                                                                                                                                                              LEFRA: 510-65-3542
INFORMATION FOR SEQ 15 NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 352 amino acids TYPE: amino acids TOPOLCGY: linear
                                                                                                                             NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 099
TELECOMMUNICATION INFORMATION:
TELEPHONE: $10-601-2585
TELEPAX: 510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 352 amino acids TYPE: amino acids
      12-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 25.6%
Matches 44, Conservative
                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-08-854-764-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94608
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Farrell, F.
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SCHATZER 2006-1893
CCMBUTER READABLE FCRN:
NEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAVE: Farrell, Kevin M.
RAGISTRATION NUMBER: 35,505
REFRENCE/DOCKET NUMBER: MIT-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 207-363-058
TELEPAX: 207-363-058
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                  ADDRESSEE: Kevin N. Fa
STRET: P.O. Box 999
CITY: York Harbor
STATE: Maine
COUNTRY: U.S.A.
ZIF: 03911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-09-091-725-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38-08-487-203A-2
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Best Local Similarity 24.8%; Fred. No. 0.0001;
Matches 38; Conservative 38; Mismatches 47; Indeis 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Compatible
OPERATING SYSTEM: PC Compatible
OFFIGER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/005,002C
FILING DATE: US/08/005,002C
FILING APPLICATION DATA:
APPLICATION DATE: US/07/789,915
FILING DATE: G8-NCV-391
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 15,505
REPERENCE/DOCKET NUMBER: 35,505
REPERENCE/DOCKET NUMBER: XIT-509LAAZ
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                      Sequence 2. Application US/08C55002C
Fatent No. 5494818
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Baker, Rohan T.
APPLICANT: Varsiavsky, Alexander
ITLE OF INVENTION: Ubiquitin-Specific Proteases
NUMBER OF SEQUENCES: 9
CORRESPENDENCE ADDRESS:
ADDRESSEE: Revin M. Farrell, P.C.
STREET: P.O. Box 939
CITY: York Harbor
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104 RVD-LSSHTLPVDSVGLAVILDTDSKRDSEAAR 135
                                           12: RLNRLAAHP------PFASWRNSEEAR 141
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Sequence 2, Application US/08487203A
Parent No. 5689904
GENERAL INFORMATION:
APPLICANT: Baker, Rohan T.
APPLICANT: Tobias, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 207-363-058
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1121 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                            Maine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 03911
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                                                                                                                           US-08-005-002C-2
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61 LEQQSIVHIVORPRARSHETNA------------SGGDHPQSTSEGSIWESRSUT 103
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Best Local Similarity 24.8%; Pred. No. 0.0001;
Matches 38; Conservative 38; Misharches 47; Indels 30;
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Patent No. 6329.41
SEMBRAL INFORMATION:
EMPEDICANT:
TITLE OF INVENTION: and recombinant DNA for use therein
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster llp
STREET: 200C Pennsylvania Avenue, N.W.
CITY: Washington
STREET: DC
                                                                                                                                                                                                                                                                                                                       MEDICM TYPE: Floppy disk
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
COMPATING SYSTEM: PC-DOS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUREENT APPLICATION DATA:
FILING DATE: 37.03N-1995
CLASSIFICATION: 435
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/005,002
FILING DATE: 15.JAN.1993
ATTORNEY/AGENT: NPFRMATION:
APPLICANT: Varshavsky, Alexander
TITLE OF INVENTION: Ubsquitin-Specific Proteases
NIXMER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 RVD-LSSHTLPVDSVGLAVILDTDSKRDSEAAR 135
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PREVENTION OF
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28.2%; Eved No. 1.6e-35;
acive 28; Mismatches 37; Indails 17; Gaps
                                                                                                                                                                                                                                                                                                                                Chery March 5.0%; Score 128; DR 2; Length 128; Space 128; DR 2; Length 128; Space 120-04; Similarity 5.2%; Fred. No. 1 68-05; Indels 10; Gaps Matches 37; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Reed, Keeven G.

APPLICANT: Reed, Michael C.

APPLICANT: Lodes, Michael C.

APPLICANT: Hodes, Michael C.

TITLE OF INVENTION: GAYMOOD L.

TITLE OF INVENTION: COMPCUMDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DEQQSTVHIVQRERSHETWASGCDRP--OATSEGSIWERRSITR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 IQKESTLEDVLEDÅ-----GGVNEPTLEADAKKYNWEKKVGRR 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-LOSC/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CLASS-FIGATION TASA
ATORNEY/AGBNT INFORMATION:
NAVE: Mak, David J
REGIS-FRATION NUMBER: 21.3121.42201
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-834-306-41
Seguence 41, Application US/08834306
Falent No. 4084135
REFERENCE/DOCKET NUMBER: 2121
TELECOMMINICATION INCRMATION:
TELEPHONE: (2.66, 6.22-4900
TELEFAX: (2.66, 6.92-691
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: maino acid
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INFORMATION POR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Bost Local Similarity 29.2%;
Matches 31; Conservative
                                                                                                                                                                      LENGTH: 128 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
                                                                                                                                                                                                                                                      ; TOPCLOGY: linear
US-08-557-3098-41
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ZIP: 98104-7092
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STATE: Washing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 VILDTBSKRDSBAARGPVKPTYNSFF1YCKGPCHKVQPG------KLRVQCGTCKQAT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 -----YKVDSD---GKIK-----RLRRECFQPQCGAGIFWAFHSNRQTCGKC-GLT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MOLEVKTLIGKTITLEVESSDTIDNVKAKIQDKEGIPEDQQRLIFAGKQLEDGRTLSDYN 60
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Patent No. 591672
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Michel J.
APPLICANT: Codes, Michel J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: RAYMOND L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4: Length 158:
  OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.C, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/09/591,725
FILING DATE: 23-DEC-1996
CLASSIFICATION DATA: 435
PRIOR APPLICATION NAMER: EP 95233620.3
FILING DATE: 22-DEC-1995
FILING DATE: 12-DEC-1995
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: E. VICTOR DOGABUSE: 85492
INFORMATION NUMBER: 35,492
INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/557,309B
FILING DATE: 14-NOV-1995
CLASSIPICATION: 435
ATTORNEY AGENT INFORMATION:
REGISTRATICN NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.0%; Score 129.5; DB 4
24.7%; Pred. No. 1.5e-05;
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COMPUTER READABLE FORM:
MEDICK TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                       : 158 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 24.7
Matches 46, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / MOLECULE TYPE: protein US-09-091-725-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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Protein Products
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                                                                                THE DETECTION AND PREVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 99. Application US/09482611B
Sequence 99. Application US/09482611B
Sequence 99. Application US/09482611B
Sequence 99. Application US/09482611B
Senent No. 6448391
Select No. 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MIVEVRENSSYGEPVEVDSOTSILQLKEVVAKROGVPADQLRVIFAGKELPNHLTVQMCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LEGOSIVAIVORPRRESHAMMASGGDEPOSTSEGSIWESRSLIRVDLSSHTLPVD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IOKESTLHIVLRIR------GGGSAVKRV-----GRRIKKLDRKIDRIGVD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LEQQSIVHIVORPRRSHETNASGGDEP--QSTSEGSIWESRSLIR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.0%; Score 128; DP 4; Length 128; 29.2%; Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 IQKESTLHLVLRLR------GGVMEPTLEALAKKYNWEKKVCRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 28.7%; Pred. No. 1.3e+05;
Matches 33; Conservative 26; Mismatches 41;
APPLICANT: Smith, John X.
APPLICANT: McNeill, Particia C.
ITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE ITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE REFERENCE: 21012. 422C3
FILE REFERENCE: 21012. 422C3
CURRENT PELICON NUMBER: US/09/256,976
CURRENT PILLON DATE: 1999-02-24
NUMBER: PARENTEIL VOIT: 2.0
SEQ ID NO 4:
LENGTH: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Ubiquitin-Lytic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence [10], Application US/09482611B
Parent No. 6448391
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Trypanosoma cruzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.0%
Best Local Similarity 29.2%
Matches 31, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-256-976-41
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                 1 MOIFVKTLTGKTIALEVESSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLADFYN 60
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APPLICANT: Skekky, Yasir A.W.
APPLICANT: Jodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Smith, John M.
APPLICANT: Smith, John M.
TILLE CP. INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.0%; Score 128; DB 3; Length 128;
29.2%; Fred. No. 1.6e-55;
iive 28; Mismatches 37; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LEQUSIVHIVORPRRSHETNASGGDEP--QSTSEGSIWESRSLTR 104
                                                                             61 LEQQSIVHIVQRPRRRSHETNASGGDEP--QSTSEGSIWESRSLTR 104
                                                                                                                              61 IQKESTLHLVLRLR------GGVMEPTLEALAKKYNWEKKVCRR 98
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0, Version #1.30
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ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Versi:
APPLICATION NUMBER: US/C8/993,674A
FILING DATE: 18-D5C-1997
CLASSIRICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKE, David U.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121,42202
TELEPHONE: (206) 627-40^
                                                                                                                                                                                                                                                                                                              Sequence 41, Application US/08993674A
Patent No. 6228372
GENERAL INFORMATION:
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APPLICANT: Skeiky, yasır A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 682-6031
INFORMATION FOR SEC 10 NC: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 126 aminc acids
TYPE: aminc acids
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Best Local Similarity 29.2%
Matches 31, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS ADDRESS ADDRESSEE: SEED and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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STREET: 6300
TTY: Seattle
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US-08-993-674A-41
                                                                                                                                                                                                                                                  RESULT 12
US-08-993-674A-41
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US-09-256-976-41
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APPLICANT: Belknap, William
TITLE OF INVENTION: Ubiquizin-Lytic Peptide Fusion Gene Constructs, Protein Products
TITLE OF INVENTION: Ubiquizin-Lytic Peptide Fusion Gene Constructs, Protein Products
File Repeace 2003-149
File Repeace 2003-149
CURRENT PROVED 2003-149
CURRENT FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US C8/801,028
PRIOR FILING DATE: 1994-07-21
PRIOR FILING DATE: 1994-07-22
PRIOR FILING DATE: 1994-07-22
SOFTWARE: Patentin Version 3-1
SEQ ID NO 101
TYPE: PI
CRGANISM: Artificial Sequence
FRANCE PRIOR CRGANIZION: Ubiquizin-Lyzic Peptide
US-09-462-6118-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.0%; Score 127.5; DB 4; Length 101; Best Local Similarity 28.7%; Pred. No. 1.3e-05; Matches 33; Conservative 26; Mismatches 41; Indels 15.
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g 3

1 MIVEVREMSSYGEPVEVDSOTSILQUKEVVAXROGVPADQLRVIFAGKELPNHLTVONGO 60

61 IQKESTLHLVLRLR-----GGGSAVKRV-----GRRI

Search completed: October 21, 2003, 21:32:19 Job time : 22 secs

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USTICE 297 2437 2 Sequence 2, Application US/10239249
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4550, Ap
820, App
6, Appli
44, Appl
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2570
1 MIVFVRFNSSYGFPVEVDSD......CWNCGCEWNRACXGDEWFDV 464
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| cgr2_6/ptodata/1/pubpaa/USS7_PJBCCMB.ppp: 4
| cgr2_6/ptodata/1/pubpaa/USS6_NSW_PUB.ppp: 4
| cgr2_6/ptodata/1/pubpaa/JSS6_NSW_PUB.ppp: 4
| cgr2_6/ptodata/1/pubpaa/USS6_NSW_PUB.ppp: 4
| cgr2_6/ptodata/1/pubpaa/USS6_NSW_PUB.ppp: 4
| cgr2_6/ptodata/1/pubpaa/USS6_NSW_PUB.ppp: 4
| cgr2_6/ptodata/1/pubpaa/USS8_PUBCCMB.ppp: 4
| cgr2_6/ptodata/1/pubpaa/JSS8_PUBCCMB.ppp: 4
| cgr2_6/ptodata/1/pubpaa/USS9_PUBCCMB.ppp: 4
| cgr2_6/ptodata/1/pubpaa/USS6_PUBCCMB.ppp: 4
| cgr2_6/ptodata/1/pubcc_2-puBCCMB.ppp: 4
| cgr2_6/ptodata/1/pubcc_2-puBCCMB.ppp: 4
| cgr2_6/ptodata/1/pubcc_2-puBCCMB.ppp: 4
| cg
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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2 US.10-239-249-2
2 US.10-239-249-2
3 US.09-864-361-36750
3 US.09-149-407-2
3 US.10-149-407-2
4 US.10-149-407-2
5 US.09-164-864-902
5 US.09-764-864-902
6 US.09-764-864-902
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 200000000
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Score Match Length DB
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Maximum DB seq
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Perfect score:
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No.
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Sequence 86, App. Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 6, Appli Sequence 7, Appli Sequence 1, Appli	FOR REGULATING THE ACTIVE	Length 156; Indels 0: Gaps 0 CWEDVLIPNRWSGECQSPCP 201 CHILL: HILL: HILL CWEDVLIPNRWSGECQSPCP 68 CWEDVLIPNRWSGECQSPCP 68 ICTOVRSPVLVFGCNSFHVICLD 128 ITDVRSPVLVFGCNSFHVICLD 128
US-09-987-107-46 US-10-128-714-8049 US-10-1296-770-2 US-10-296-770-2 US-10-396-770-2 US-10-396-770-2 US-10-396-770-3 US-10-396-770-3 US-10-396-770-3 US-10-386-712-3 US-10-366-153-6 US-10-366-153-6 US-10-366-153-6 US-10-366-153-6 US-10-366-153-6 US-10-366-153-6 US-10-366-153-6 US-10-366-153-6 US-10-366-153-6 US-10-368-971-8 US-10-189-971-8 US-10-189-971-4 US-10-189-971-4 US-10-189-971-4 US-10-189-971-4 US-09-986-166-US-09-986-166 US-10-189-971-4 US-10-189-971-4 US-10-189-971-4 US-09-986-166-US-09-986-166 US-10-189-971-4 US-10-189-971-4 US-10-189-971-4 US-09-986-166-US-09-986-166 US-09-986-166-US-09-971-4 US-10-189-971-4 US-09-986-166-US-09-971-4 US-09-986-166-US-09-971-4 US-09-986-166-US-09-971-4 US-09-986-166-US-09-971-4 US-09-986-166-US-09-971-4 US-09-986-166-US-09-076-US-09	ALIGNXENTS 65548 ICALS, INC. ONS THAT CAN BE USED 209/785,548	Score 744; DE 10; Pred. No. 1.4e-61; BY Mismatches 11; CALCACHTHAGGE INCLINICATION OF 11; CALCACHTHAGGE SWALNLITSWARSIPCIAGE SWALNLIAINSPHITCITC TGYSLPCY 289 CACASTPCY 156 CACASTPCY 156
80000000000000000000000000000000000000	26 11 29	28 29 20 20 20 20 20 20 20 20 20 20 20 20 20
11.08 1.13 1.13 1.13 1.13 1.13 1.13 1.13 1.1	UC-09-785-548-4 Sequence 4, Application US/0 Sequence 4, Application US/0 Patent No. US202015577A1 GENERAL INFORMATION APPLICANT: AVENTIC PHARMACE TITLE OF INVENTICN: COMPOSI FILE REFERENCE: ST00005 CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 201- NUMBER OF SEQ ID NOS: 46 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 4 CLENGTH: 156 TYPE: PRT CROMANISM: Hono Sapiens US-09-788-548-4	Ouery Match Bost Local Similar Matches 129: Cor Oy 142 YNSFF Cb 9 YNSFY Cb 69 GTSAB1 Cb 69 GTSAB1 Cb 7 262 CFHLYC Cb 129 GTHLYC

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WHENESSED IN PLACENTA, SIGNAL ... J. KB
WE EXPRESSED IN LING, SIGNAL ... J. KB
WE EXPRESSED IN HELA, SIGNAL ... J. 63
WE EXPRESSED IN RETA, SIGNAL ... J. 63
WE EXPRESSED IN RETA, LIVER SIGNAL ... G. 68
WE EXPRESSED IN RETAL LIVER SIGNAL ... G. 68
WE EXPRESSED IN REAIN, SIGNAL ... G. 69
WE EXPRESSED IN ADULT LIVER SIGNAL ... G. 73
WE EXPRESSED IN ADULT LIVER SIGNAL ... G. 73
WE EXPRESSED IN ADULT LIVER SIGNAL ... G. 73
WE EXPRESSED IN ADULT LIVER SIGNAL ... G. 73
WE EXPRESSED IN ADULT LIVER SIGNAL ... G. 73
WE EXPRESSED IN ADULT LIVER SIGNAL ... G. 73
WE EXPRESSED IN ADULT LIVER SIGNAL ... G. 73
WE EXPRESSED IN ADULT LIVER SIGNAL ... G. 74
WE SET HUMAN HIT: T785581, EVALUE 2. JGG+0
WE SWISSPHOT HIT: G24833, EVALUE 9.10e-01
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9.4%; Score 242; CB 9; Length 46;
Best Local Similarity 93.5%; Pred. No. 2.4e-15;
Matches 43; Conservative 0; Mismatches 3; Indels
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/20,366
PRIOR FILMO DATE: 2000-10.04
PRIOR PLING DATE: 2000-10.04
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATI
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Patent No. US20020132293A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
GRGANISM: Horo saptetts
FRATURE:
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US-09-808-387-42
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Patent No. US20020548763A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pent, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DEMIVED SINGLE EXON NUCLEIC ACID FROBES USEFUL FOR
                                                                        APPLICANT: HOWER, MARIUS
APPLICANT: HOWER, MARIUS
APPLICANT: LINK, WOLFGRANG
APPLICANT: BAUMEISTER, RALF
TITLE OF INVENTION: NEURODEGERATIVE DISEASES AND
TITLE OF INVENTION: DESCRIPTIVE DISEASES, AND METHODS FOR FINDING SUBSTANCES AND
TITLE OF INVENTION: IDENTIFICATION OF A NEMATODE GENE
TITLE OF INVENTION: IDENTIFICATION OF A NEMATODE GENE
TITLE OF INVENTION: IDENTIFICATION OF A NEMATODE GENE
TITLE OF INVENTION: 10504-00000
CURRENT FILING DATE: 2002-09-20
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 12
SEQ ID NOS: 12
SEQ ID NOS: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 SLLEPSGATSQAYRUDKRAAEQARWEEASKETIKKTTKPCPRCNVPIEKNGGCMHMKCPQ 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 ASGGDEPQSTSEGSIWESRSLTRVDLSSHTLPVDSVGLAVILDTDSKRDSEAARGPVKPT 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 SILÇLKEVVAKRÇGVPADQLRVIFAGKELPNHLITVQNCDLEQQSIVHIVQRPRRRSHETN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 YNSFFIYCKGPCHKVOPGKLRVOCGTCKQATLTLAQGPSCWDDVLIPNRMSGECQSFDCF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 20.5%; Score 528; DB 12; Length 386; Best Local Similarity 27.6%; Pred. No. 7.7e-41; Matches 123; Conservative 67; Mismatches 164; Indels 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 TSCGMDWCFKCKTEWKEECQWDHWFN 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Caenorhabditis elegans US-10-239-249-2
    US20030177507A1
Publication No. US20
GENERAL INFORMATION:
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US-09-864-761-36750
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1287 LAAGLOVHQAQAVPVRFDHOFOVOV---SFL---GODDJL9SLOOMHYCOKSOWNEYLTTR 1340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1437 NSC-----GHMSQ-WVDDGGYYDGXSVBAQSKHLAKLISKRCPSCQAFIBKNBGCLHM 1488
                                                                                                                                                                                                        271 INDROFVHDAQLGYSLPC-VAGGP----NSLIKELHHFRILGBEQYTRYQQ----YOA5 320
                                                                                                                                                                                                                                                                                                                                           321 BÖYLOMGGYLÇPRPSCGAGILPBÇGQRKVTÇBGGNĞLG-----CGFVFCRDÇK--5AYHE 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 ESGAAADDIKPOPROAAYIIKMMDGSONHMIG- AVOGOBFOWLOMKEISDUHYLSPSGC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 SPCDSLLBPSGATSQAYRVDXRAABQARWEBASKETIKKTIKPCPRCNVPIEKNGGCNEM 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 SEKETSVALNSITSNERS-----IPCLAC----TEVESPVLVFQCNHRHVICLEGF 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESQYTRYQQYGABECVLQXGGVJCPRPGCGAGLL-----PSQGQRKVTCBGGNGLGCG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 TBFCYHCKCIWHENCTCD--------AAROBRAGSLRIRKSSSISYSC 209
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   Saps
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   Indels
   91;
   Mismatches
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Publication No. US20030167109Al
GENERAL INFORMATION:
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Best Local Similarity 24.2'
Matches 75; Conservative
67, Conservative
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US-10-149-407-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 CFCEKLGSECMYFLEC--RHVYCKACLKDYFBIQIRDGQ------VQCL-NCPEPK 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 RKVTCEGGNGLGCGFVFCRDCKEAYH-----EGDCDSLLEPSGATSQA-----YRV 392
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                  APPLICANT: Kasa Paim
APPLICANT: Tools Timmusk
APPLICANT: Tools Timmusk
APPLICANT: Tools Timmusk
TITLE OF INVENTION: MAMMALIAN NEURALIZED FAMILY OF
TITLE OF INVENTION: TRANSCRIPTION REGULATORS AND USES THEREFOR
FILE REFERENCE: CERRES. 2014
CURRENT APPLICATION NUMBER: US/09/608.387
CURRENT PILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEC ID NO 42
LENGTH: 474
TYPE: PRT
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25.9%; Pred. No. 1.96-08;
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Best Local Similarity 26.0%; Pred. No. 3.2e-12;
Matches 81; Conservative 34; Mismatches 123; Indels
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APPLICANT: Scanlan, Matthew
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Gure, Ali
APPLICANT: Gure, Ali
APPLICANT: Gure, Yao-Tseng
APPLICANT: Lowelly and Applicant
CORRENT APPLICATION NUMBER: US/10/146,473
CORRENT APPLICATION NUMBER: US/0/291,150
PRICR FLLNG DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 82
SEQ ID NO 44
SEQ ID NO 44
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Publication No. US20030108689A1
GENERAL INFORMATION:
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US-09-808-387-42
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Best Local Similarity
   GENERAL INFORMATION
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106 CASCP-----KIICERE---GCQIEFCYHCKQIWHENQICDYARG----QRAGILRVRIKH 154
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                                                                                          288 CVAGCPNSLIKELHHF---RILGEBOYTRYCOYGAERCVIQMGGVLCPRPGCGAGLL--- 341
                                                                                                                                        -----PLMHKYEEFMLRRYLASDPDCRW-------CPAPDCGYAVIAYG 105
                                                                                                                                                                                        342 ----PEQSQRKVTCEGGNGLGCGFVFCRDCKEAYHEGD-CDSLLEPSGATSQAYRV-DKR 395
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---CVTRINDRQFVHDAQLGYSIP 281
                                     16 RAPRIL - SCPHRS - - CROCLRHYLRISESRVPISCPBCSERLNP-- - - HDIRLLADP 68
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; Patent No. US2002012753A1
; GENERAL INFORMATION:
A PLICANI ROSED et al.
TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TILLE REFERENCE: PT23
CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 201-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 125
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Patent No. US20020165137A;
GENERAL INFORMATION;
APPLICANT: Ruben et al.
TITLE OF INVENTION; Nucleic Acids, Proteins, and Antibodies
FILE REFSRENCE: PAL27P1
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244 RSPVIVEQCNURHVICLOCFHLY-----
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Rest Local Similarity 76.9%
Matches 70; Conservative
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JS-09 764 464-1263
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US-09-764-864-1263
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US-09-860-670-82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 TEFCYHCKQIWHPNQTCD-------AARQERAGSIRLRTIRSSSISYSQ 289
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       WS-10-149-407-4

WS-10-149-407-4

Sequence 4, Application US/10149467

Publication NO. US2033618719941

SERNEAL IMPORMATION:
APPLICANT: SOBUE, Gen

TITLE OF INVENTION NO. US20030187199Aiel Proteins and Genes
FILE REFERENCE: P22443

CURRENT APPLICATION NUMBER: US/12/149,467

CURRENT FILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-12-13

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.2

SEQ ID NOS: 4
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TILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPRENCE: PT223
CURRENT APPLICATION NUMBER: US/08/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.2%; Score 184.5; DB 1
24.2%; Pred, No. 3.1e-08;
tive 28; Mismatches 80
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-802
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Matches 75; Conserv
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US-09-764-864-802
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TILE OF INVENTION: Colon and Colon Cancer Associated Polynuclectides and Polypeptic Plane of INVENTION: Colon and Colon Cancer Associated Polynuclectides and Polypeptic CIRENT APPLICATION NUMBER: US/10/106,698
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT PILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/157.137
PRIOR FILING DATE: 1099-09-28
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-1-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
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          396 AABQARWEBASKETIKKTTKPCFRONVPIEK - NOGCMHMKCPOFCCKLBWCWNC---- 4446
                                                                                                                                      135 TSGLSYGQESGPDD1----KPCPRCSAYIIKMNDGSCNÄMTC--AVGGCEFCWLCMKEIS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCGATION: (364)
VERRE INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/REY: MISG FRATURE
LOCATION: (370)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 FPLLRAPAVDCGKGHLFCWECLGEAHBPCCCQTWKWHLQKITEKFPEELVGVS5AY---- 120
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| Patent No. US202012753A.
| GENERAL INFORMATION
| APPLICANT: Roses et al.
| TITLE OF INVENTION: Nucleic Acids. Proteins, and Amilbodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.0%; Score 179; DS 15; 26.7%; Pred. No. 3.4e-08; tive 25; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                     Sequence 4550, Application US/10106698; Publication No. US20030109690A1; GENERAL INFORMATION;
                                                                                                                                                                                                                                         209 DIRYISPSGCTFWGKKPWSR 228
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Best Local Similarity 26.78
Matches 48; Conservative
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US-10-106-698-4550
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US-09-764-864-820
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TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE FREERENCE: PAOSOER!

UNRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2032-03-27

PRIOR PELING DATE: 2000-09-29

PRIOR PILING DATE: US 60/157,137

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-12-33

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: Patentin Ver. 3:0

SEQ ID NO 4649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 TSGLSYGQESGPD51----KPCPRCSAXIIKANDGSCNAMTC--AVCGCEFCWLCXKEIS 209
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                                                                                                                                                                                                                                                                                                                                                                                                ----CVTRINDRQFVHDAQLGYSLF 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 ----PEGGGRKVTCEGGNGLGCGFVFCRDCKEAYHEGD-ODSILEPSGATSQAYRV-DKR-395
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                                                                                                                                                                                                                                                                                                                                                                                                                                               16 RAPRÍL-SOPHRS--CRÓCIRHYLRIEISESRVPISCPECSBRINP----HOIRLLIADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 CVAGCPNSLIKELHHF---RILGEEQYTRYQQYGAEECVLQMGGVLCPRPGCGAGLL---
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                                                                                                                                                                                                                                                                                        Query Match 7.1%; Score 182; DB 10; Length 617; Best Local Similarity 26.9%; Pred. No. 3.5e-08; Matches 70; Conservative 24; Mismatches 70; Indels 96
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CURRENT APPLICATION NUMBER: US/09/860,670
CURRENT FILING DATE: 2001-05-21
Frior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 289
SOFTWARE: Patentin Ver: 2.0
LENGTH: 617
TYPE: PRT
TYPE: PRT
CRGAN:SM: Homo sapiens
US-09-860-670-82
                                                                                                                                                                                                                                                                                                                                                                                           244 RSPVLVFQCNHRHVICLDCFHLY------
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US-10-106-698-4649
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US-10-106-698-4649
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73 KESTIHLVIRIRGGSIR--GROGDEPPOSFWORMVFULVVCVLKOSGRDYVSCRGSA 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 56;
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Best Local Similarity 24.1%; Pred. No. 3.59-05;
Matches 53; Conservative 37; Mismatches 64; Indels 6
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                12S CGCEPCWLCMKEISDLHYLSPSGCTFWGKKPWSH 158
                                                                                                                                                                                                                                                                                                                                          APPLICANT: GRAVERSEN, Jonas
APPLICANT: GRAVERSEN, Jonas
APPLICANT: MOESTRUP, Soren
TITLE OF INVENTION APOLIPOPRCTEINS ANALGGUSS
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US,09/987,107
CURRENT APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-15
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Job time : 72 secs
                                                                                                                                                                                                                                     Sequence 44, Application US/09987107; Patent No. US/09020156007A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                             RESULT 15
US-09-987-107-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 YCVTRLNDRQFVHDAQLGYSLPC-VAGCP----NSLIKELHHFRILGEECYTRYQQ---- 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 - YGABECVLQMGGVLCPRPGCGAGLLPEQGQRKVTCEGGNGLG-----CGFVFCRDCK-- 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 GY-VESC---SNLTWCTNP------QGCERILCRQGLGCGTTCSKCGWASCFNCSFP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 BAYHEGDCDSLLEPSGATSQAYRVDKRAAEQARWEEASKETIKKTTKPCFRCNVPIEKNG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 EAHYPASC-----GHMSG-WVDDGGGYYDGMSVEAGSKHLAKLISKRCPSCQAPIEKNE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 CPRPGCGAGLL-----PEQGQRKVICEGGNGLGCGFVFCRDCKEAYHEGD-CDSLLEP 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 SGATSQAYRV-DKRAAEQARWEEASKETIKKTTKPCPRCNVPIEK--NGGCMHMKCPQPQ 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 -- ORAQILRVRIKHISGLSYGQESGPDD1----KPCPRCSAYIIKMNDGSCNHMTC--AV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 YLTTRI-----EQNLVLNCTCPIADCPAQPTGAFIRAI----VSSPEVISKYEKALLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 CPAPDCGYAVIAYGCASCP----KLTCBRE---GCCTEFCYHCKGIWHPNOTCDMARQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.6%; Score 169.5; DB 19; Length 431; Best Local Similarity 27.5%; Pred. No. 3.1e-07; Matches 56; Conservative 24; Mismatches 73; Indels 51;
FILE REFERENCE: PT223
CURRENT APPLICATION VMBER: US/09/764,864
CURRENT FILING DATE: 2601-01-17
Prior application data removed - consuit PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 823
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Best Local Similarity 36.5%; Pred. No. 3.1e-06;
Matches 47; Conservative 16; Mismatches 44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440 CKLEWCWNC-----GC-----EWNR 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           429 GCMHMKCPQPCCKLEWCWNCGCEW 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 GCLHMTC--AKCNHGFCWRCLKSW 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/0996194
Patent No. US20020151696A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     LENGTH: 431

TYPE: PRT

CRGANISM: Homo sapiens
US-09-764-864-820
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ORGANISM: homo sapiens
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A; Gene: CESP: K08E3.7
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protein kinase C-i
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                                          October 21, 2003, 21:24:45; Search time 43 Seconds (without alignments) 1037.727 Million cell updates/sec
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                                                                                           ......CWNCGCEWNRACMGDHWFDV 464
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                             protein search, using sw mode]
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JC5983
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Gapop 10.0 , Gapext 0.5
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3: pir3: *
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Match
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172.5
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ubiquitin / riboso
ubiquitin - Autogr
ubiquitin precurso
polyubiquitin [1]
ubiquitin / riboso
polyubiquitin [7]
                            ALR protein - huma
probable unquitin
hypothetical prote
probable RING zinc
hypothetical prote
OMF MSV444 probabl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Symmitted to the EMBL Data library, November 1996
A;Reference number: 219743
A;Reference number: 219743
A;Reference number: 219746
A;Status: preliminary; translated from GB/EMBL/DD3J
A;Molecule type: DNA
A;Residues: 1-357 <WIL>
A;Cross-references: EMBL:28:568; PIDN:CABC4599:1: GSPDB:GN00021; GESP:K08E3.7
A;Experimental source: clone K08E3
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379 LIEPSGATSGAYRYDKRAAEGARWEBASKETIKKTTKPOPRONVPIEKNGGOMHMKCPQP 438
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Cybeckes Caenorizabditis elegans
Cyate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999
CyAcoesson: 723466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 CV-LQMGGVLCPRFGCGAGIL--PEQGQRKVTCEGGNGJGCGFVFCRDCKEAYHRGDCDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 SILQLKEVVAKRQGVPADQLRVIPAGKELPNHLTVQNCDLEQQSIVHIVQRPRRSHETN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 ASGGDEPQSTSEGSIWESRSLTRVDLSSHTLPVDSVGLAVILDTDSKRDSBARGPVKPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 LGSFYVWCKN-CODVVKRGKLRVYCQKCSSTSVLVKSBPQNWSDVLKSKRIPAVCBECCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 GTRABFFFROGAHPTSDKETSVALNLITSNRRSIPCIACTOVRSPYJVFQCNHRHVICLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 LIAVDDKGVTCPNVSCGQSFFWEPYDDDGRSQCP----BCFFSFCRKC---FERNCVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 YNSFFIYCKGPCHKVQPGKLRVQCGTCKQATLITAQGPSCWDDVLIPNRMSGBCQSPDCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----RVVQDVEHFHIMGQTSYSEYQRKATER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query March 18.7%; Score 481.5; DB 2; Length 357; Best Local Similarity 25.6%; Pred. No. 6.1e-30; Matches 114; Conservative 61; Mismatches 151; Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 3
A;Introns: 23/3: 72/2: 215/1; 286/2; 311/2
                         77.03.45.4
17.03.45.4
17.03.45.3
17.2.63.45.3
17.2.63.45.3
17.0.5.45.3
17.0.5.45.3
17.0.5.45.3
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Rest Local Similarity 27.2%; Pred. No. 9.36-10; 	Oy 234 SIPCIACTDVRSPVLVFQCNARHVICLDCFHLYCVTRINDRQFVHDAQLGYSLFC 288	Qy 289 VAGCPNSLIKELHHFRILGEBOYTRYQQYGABECVLQMGGVLCPRPGGAGLLPE 343	2y 344 QQQRKVTCEGGNGLG	233 OV 203	267 IFKNODESENKNWMLANSKPCPECKRPIEKNOGNYMTCSAP-CGHEFOWICLKAYRRHS	OY 455 - AC 456	 T02366 hypothetical protein T8F5.21 - Arabidopsis thallana Cispecines: Arabidopsis thallana (mouse-ear cress) Cispecines: Arabidopsis thallana (mouse-ear cress) Cispecines: Arabidopsis thallana (mouse-ear cress)	C.Accession: T02366 Rivysorskala, V.S., Schwartz, J.R., Toxiumi, M., Yu. G., Kwan, H., Liu, S., Ji, C., Li, Y., Palm P., Shimm P., Sum H., Davis, P. W., Schwar, J.P., Endersefel, M. E.,	19 1999 - 1 8AC 1885 COURT SECTION OF THE SECTION O		A.Molecule type: DNA A.Residues: 1-644 e.VVSs A.Residues: 1-644 e.VVSs A.Cross erreferences: EVDL.A.Coo45.2 NTE-03335931 P.D.c3333547 GSPD-GROOF9 ATCD-C		21/3: 25	Ouery Match Ouery Match Best Local Similarity 27.4%; Pred. No. 3.78-09; Matches 68; Conservative 32; Mismatches 98; Indols 50; Gaps 14;	215 PISOKDISVALMLITSNRASIPCIACTOVRSFVLVPOCNHRHVICLDCFHLVCVIRLM	DB 121 PTDGENSAVSF	Cy 273 DRQFVHJAQLGYSLPCVAGGFNSLIKELHHFRILGEEQYTRYQQYGAEECVLGMG 327	2y 328 GVLCPREGGGAGLLFEQGORKUTCEGGRGLGCGFVFCRDC-KEAYHEGDCDSLLEPSG 384	Cy 385 AISCAYRUDKRAABQARWEBASKETIKKTIKPOPRONVEJEKNOGOMHMKOPQPOCKLEW 444	445 CWNCSCEW 452		RESULT 5 GB7793	protein C27A12.7 (imported) - Caenorhabdinis elegans
2y 439 QCXLEWCWNCGCEWNRACMCDHWPD 463	RESULT 2 F87783	protein C27A12.6 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001 C:Acceston: F8779		oio b) .	147CD.	Query Match Best Local Similarity 26.1%; Pred. No. 5.6e-10; Matches 74; Conservative 35; Mismatches 94; Indels 80; Gaps 17;	Cy 206 BFFFKGGAHPISSXDISVALNLITSNRRSIPCIACTDVRSPVLVFQCNHRHV 257	44	Cy 258 ICLDCPHLYCVTRINDRQFVHDAQLGYSLPCVAGCPNSLIKELHHFRILGEEQYTRY 314 : :	OY 315QQYGABECVLCMGGVLCPRPGGAGLDPEQGQ-RKVTCEGGNGLGCF 361	188 PTMVSKYRKLMVASYVEINCLLRWCPGIDGGKAVKVSHWEPRLVVCSCGT 23	JY JACKDURANTEG-DCDSLLEPGGATSQAYRVDKBAAEQARWEFASKETIKKTTKPCRFC 420 238 CFCFSCGQWWHEPLNCRH	QY 421 NVPLEXNGGCMEMKCPQPQCKLEWCWNCGCEWNRACMG 458		M25CL1 3 H84724	probable ARI-like RING zinc finger protein [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001	Rillia (M. 1.) Town, 1972, Rounsley, S.D., Shea, T.P., Benito, M.I., Town, C.D., Fujii, C.Y., M.; Koo, H.; Noffat, K.S., Cronin, L.A., Shen, M.; VanAken, S.E., Umayar, L., Tallon, L. euss, D., Nierman, W.C., White, C., Eisen, J.A., Salzberg, S.L., Fraser, C.X., Venter, J	Nature 402, 761-768, 1999 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:18617197 A:Accession: PA4724	A;Status: preliminary A;Molecule type: DNA	A;Residues: 1.543 <sto> A;Cross_references: GB:AE002093; NID:g4887759; PIDN:AAD32295.1; GSPDB:GN00139 C;Genetics:</sto>	A; Map position: 2	Query Match 8.7%; Score 224.5; DB 2; Length 543;

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process C27A12.8 [imported] - Caenoxhabditis elegans
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A,Accession: 3644224
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AlGross-references: GB:ABCOL093; NID:Q4887746; PIDN:AAD32296.1; GSPRB-GNC0139
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Rest Local Similarity 25.1%; Pred. No. 4.7e-18;
Aatches 69; Conservative 36; Mismatches 109; Indeis
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001
S;ancorymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating blotod A;Reference number: A75000; MUD: 99069613, PMID: 9951916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: Garmanary
A;Accession: Garmanary
A;Residue: pre: DNA
A;Residue: 1497 <STO>
A;Residues: 1-497 <STO>
A;Cross-references: GB:chr_I; PIDN:AAB93644.1; PID:g2105479; GSPDB:GN00613; CESF:G27A12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 HPTSDKDTSVAL---NLITSNRRSIP-----CIACTDVRSPVLVFQCNHRHVICLDCFHL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 HP----DTIAFLIDAQVIPRQQEVIPAGDAECDICCSM-DELSGLSCNHR--ACABGWGA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 YCVTRINDRQFVHDAQLGYSIPCVAGCPNSLI.----KELHHPR---ILGBEQYTRYQQY 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 YLTNKI-----VSDAQ--SEIECMA--PNCKLJIEDEKVLAYIKDPTIIAKYRKMMVASY 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 GABECVLQMGGVL--CPRPGCGAQLLPEQQQ-RKVTCEGGNGLGCGFVFCRDCKEAYHEG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 -----IBINALLKWCPGVDCGRTVKVSHGEPRLVVCT-----CGSRFCFSCGQDWHEP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 -DCDSLLEPSGATSQAYRVDKRAAEQARWEEASKETIKKTTKPCPRCNVPIEKNGGCMHM 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 PGCGAGLLPE--QGQRKVTCEGGNGLGCGFVFCRDC-KEAYHEGDCDSLLEFSGATSQAY 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PGCDSAVEYDLGSGSYDVTC-----CCSFSFCWNCTEEAHPPVDCDTV------43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----AKWILKNSAESENMNWILANSKPCPKCKRPIEKNQGCMHMTC-TPPCKFEF 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein - curled-leaved tobacco (fragment)
C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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7.9%; Score 202.5; DB 2;
Best Local Similarity 34.6%; Pred. No. 2.9e-0E;
Matches 47; Conservative 14; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.9%; Score 254; DB 2; Best Local Similarity 26.3%; Pred. No. 3.5e-08; Matches 68; Conservative 34; Mismatches 95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 KCPOPOCKLEWCWNCGCEW 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 TCKNTGCKFQFCWMCLGPW 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 VNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A: Map position: 1
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Cipecies: Homo sapiens fman:
Cipacies: Homo sapiens fman:
Cipaces: Accession: 100350 #sequence_revision 01-Feb 1999 #text_change 21-Jui-2000
CiAccession: 100350 #sequence_revision 01-Feb 1999 #text_change 21-Jui-2000
Brishkawa, K.; Nagase, T.; Suyama, M.; Miyajina, N.; Tanaka, A.; Kotani, H.; Nomura,
DNA Res. 5: 169-176, 1996
Alther Frediction of the coding sequences of unidentified human genes. X. The comple
A.Accession: 103350
A.Accession: 103350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1341 I -----ECNLVINCTCPIAOCPACPTGAFIRAI----VSSPEVISKYEKALLRGY-VE 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 LNDRQFYHDDQLGYSLPC-VAGCP----NSLIKELHHFRILGESQYTRYQQ-----YGAR 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 SEVKM--KOSECPHCHRMVCVEGGTQWHPBMTCEEFQKL--KANBRGRDD15LATMAK-- 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A/Cross-references: EMSL:ABC14608; NID:g3327229; PION:BAA31683.1; PID:g3327230
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                                                                                                                                                                                                                                                                                                                                                                                                                                   229 ISNRRSIPCIACIDVRSPVLVRQ---CNHRHVICLOCFHLYCVTRLNDRQFVHDAQLGYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPC-VAGCPNSLIKELHHFRIJGERQYTRYQQYGAEECYLQMGGVLCPRPGCGAGLLPRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 SSKTATFDCEICVDSKSIIESFRIGGCSHFY--CNDCVSKYIAAKLQONIL-----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 IECPVSGCSGRLEPDQCR-CILPKEVFDRWGDALCEAVVMRSKKFYCPYKDCSALVFLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 GQRXVICEGGNGLGCGFVFCRDCKEAYH-EGNCDSLLEPSGATSQAYRVDKRAAEQARWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 VALNLITSNRRSIP-----CIACTDVRSPVLVFQCNH------RHVICLDCFHLYCVTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1287 LAAGUCVHQAQAVPVRPDHCPVCV---SPL---GCDDDLPSLCCMHYCCKSCWNBYLTTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 ECVLOMGGVLCPRPGGGAGLLPEQGGRKVTCEGGNGLG-----CGFVFCRDGK- EAYHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1437 ASC-----GHMSQ-WVDDGGYYDGKSVÄAQSKHLAKLISKRGPSGQAPIEKNEGCLHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69; Gaps
                                                                                                                                                                                                                                                                                                                                                                                          32;
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                                                                                                                                                                                                                                                                                                                                                                                       indels
                                                                                                                                                                                                    A:Experimental source: cultivar Columbia; BAC clone F4P12
unmitting to the Protein Sequence Database, January 2000
A;Reference number: 223016
A;Accession: 745909
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 27.4%; Pred. No. 5.5e-08;
Matches 62; Conservative 37; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.5%; Score 191.5; CB 2; 25.9%; Pred. No. 1.30-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein KIAA0709 - buman (fragment)
O(Species: Homo sapiens (man)
                                                                                                          A;Status: preliminary
A;Molacule: type: DNA
A;Residues: 1-320 <BLO>
A;Cross-references: EXBL:AL132966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 25.9%
Matches 67, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Experimental source: brain C)Genetics:
A,Note: KIAA0708
                                                                                                                                                                                                                                                A;Map position: 3
A;Introns: 295/2
A;Note: F4P12.390
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                                                          77; Gaps 13;
                                                                                                          292
                                                                                                                                                      161
                                                                                                                                                                                                                                                                                                                                                                                397 ABÇARW-----BEASKETIKKTTKPCPRCNVPIBKNGGCMHYKCPQPQCKLEWCWNCGC 450
                                                                                                                                                                                                                                                                                                                                                                                                                292
                                                                                                                                                                                                                                           LRVKCPEPSCYAVVGQDMIDEVTEKKOKDKYYRYFLRSYVEDGKKMKW----CPSPGCEC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 PNSLIKELHHFRILGE-------EQYTRY--QQYGAEECVLCMGGVLCPRPGCGA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 LRVKCPEPSCYAVVGQDMIDEVTEKKDKDKYYRYFLRSYVEDGKKWKW----CPSPGC-- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 GLLPEQGQRKVTCE-GGMGLG------CGFVFCRD-CKEAYHEGDCDSLLEPSGATSQA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-542 <STO>
A;Cross-references: GB:AEC02093: NID:g4887758; PIDN:AAD32294.1; GSPDB:GN:0139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390 YRVDKRAAEQARWEEASKETIKKTTKPCPRCNVPIEKNGGCMHMKCPQPQCKLEWCWNC 448
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                                                                                                                                                                                                                                                                                                                    235 IPCIACID--VRSPVLVFQCNHRHVICLDCFHLYCVTRLNDRQFVHDAQLGYSLPCVAGC
                                                                                                                                                                                               293 PNSLIKELHHFRILGE-------EQYTRY--QQYGAEECVLQMGGVLCPRPGCGA
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7.8%; Score 201; DB 2; Length 542;
Best Local Similarity 25.5%; Pred. No. 6.5e-08;
Matches 61; Conservative 31; Mismatches 75; Indels
                                                                                                                                     119 IQCGICFESYTRKEIASVSCGHPY--CKTCWTGYITTKIEDG-----
                                                            Indels
                               Local Similarity 23.9%; Pred. No. 5.6e-08; tes 60; Conservative 32; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            451 EWNRACMGDHW 461
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CY 232 RRSIPCIACTOVR-SPVLVPQCNHRHVICLDCPHLYCVTRLNDRGFVHDAQLGYSLPCVA 290 	GAEECVLQMGGVLCPRPGCGAGLL 	342 PEQGORKVT	397 AEQARWEEASKETIKKTTKPOPRONVPIEKNGOOMBINKOPOPOCKLENOWVGGGENNRAG 45	321 VKKÄRKE	37 457 MODHWF 462 	RESULT 14 131653 hypothetical protein Y57A:0A.ff - Caenorhabdinis elegans	. Cippelles: CaenormapOliis elegans CiDate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Cct-1999 CiAccession: 711653 R.S.We. R.	submitted to the EMBL Data Library, Septembor 1999 A,Reference number: Z21048 A,Accession: T31653	A;Status: preliminary; Iransiated from GB/EMEL/DDBS A;Molecule type: DNA A;Residues: 1-1048 <mil> A;Residues: 1-1048 <mil> A;Cross-references: EMBL:All17195; NID:e1549722; PIDN:CAB55036.1: CESP:Y57A10A.ff A;Experimental source: clone Y57A10A</mil></mil>	C:Genetics: A/Gene: CSSP:Y57AiOA.ff A/Introns: 34/1; 82/3; 156/3; 398/3; 556/3; 796/1; 863/3; 1024/1	Query Match 7.3%; Scoxe 187.5; DB 2; Length 1048; Best Local Similarity 22.3%; Pred. No. 1.5e-06; Matches 59; Conservative 59; Mismatches 148; Indels 137; Gaps 26;	5: PNHLTVQNCDLBQQSIVHIVQRPRRRSHBTNASGGDBPQST-SBGSINBSRSLTR	Oy 105VDISSHTLPVDSVGLAVILDIDSKRBSBAARGPVKETYNSFFIYCKGPCH 154	Oy 155 KVOPGKLRVQCGTCKQATLTJAQGPSCWDDVLIPNRMSGBCQSPDCPGTPABF 207	206 PPKGGAHPTSDK3VALNLITSMRRSIPCIACTDVRSPVLVPQCNHRHVICLDGFHLYC 267	2y 268 VTRIADAQLGYSIRC-VAGGPASI	Cy 312 TRYCOYGABECVLOMOGVL - CPRPGCGAGLPFGGGGRKVT CEGGNGLGGGFFCR 365 	366 DCKEAYHEGDCDSLLEPSGATSOAYRAAFQARWEEASKETIKKITKPCFRCVPTE
Qy 434 KCPQPQCKLEWCWNCGCEW 452 	RESULT 12 116477 hypothetical protein FS6D2.5 - Caenorhabditis elegans	C,Species: Caenorhabditis elegans C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C:Accession: T16477 P.Du. 7	Submitted to the EMBi Data Library, August 1994 Albescription: The sequence of C. elegans cosmid ₹5652. AlReference number: 218519	A;Accession: T16477 A;Status: preliminary; translated from G3/EMBL/DDBJ	A/Rolecule type: DNA A/Rossidues: 1-437 <002> A/Cross-references: EMBL:U13644; NID:g532:00; PID:g1945502; PIDN:AAB52683.1; GSPDB:GNOOD A/EXperimental source: strain Bristol N2; clone F56D2	U.Membellos C V.Gene: CESP:F56D2.5 A.Map position: 3 A.Introns: 41/3: 134/3: 185/3: 223/3: 254/2: 287/2: 414/3	Query Match 7.4%; Score 191; DB 2; Length 437; Best Local Similarity 21.0%; Pred. No. 3.1e-07; Matches 62; Conservative 46; Mismatches 111; Indels 76; Gars 15;	211 CGAHPTSDKDTSVALNLITSNRRSIPCIACTDVRSPVLVFQ-CNHRHVI 2	259	CY 314 YQQYGAEECVLQMGGVL-CPRFGCG-AGLLPEQGQRKVTCEGGNGLGCGFVFCRDCKEAY 371	372 HEGDCDSLLEPSGATRQDKRAAEQARWBEASKE:	3 2 9 8 8 9 9 8 9 9 9 9 9 9 9 9 9 9 9 9 9	RESULT 13	Siguse Siguse de protein YKR017c - yeast (Saccharomyces cerevisiae) Cispecies: Saccharomyces cerevisiae Cispecies: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002	C;Accession: 538086 R;Juesterhoeft, A.; Moestl, D.; Poehlmann, R.; Philippsen, P. submitted to the Protein Seguence Database, March 1994 A;Reference number: S37811	A)Addession: S38696 A)Modesule type: DNA A)Residues: 1-551 aDUE A)Cross-references: BMBL:228242; NID:9486434; PID:9486435; GSPDE:GN00011; MIFS:YWR0100	A,Experimental source: strain S286C C,Gonetics: AA:Genetics: AA:Asne: XIPS:YKR017c A;Cross-references: SGD:S0021725	A:Map position: 11R Query Match 7.4%; Score 189; DB 2; Length 551; Best Local Similarity 24.6%; Pred. No. 5.7e-07;

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A:Status: preliminary, translated from GB/EMBL/DDBJ
A:Aclecule type: DNA
A:Residues: 1-816 cJGH>
A:Residues: 1-816 cJGH>
A:Cross-references: EMBL:U80847; PIDN:AAB37987.1; GSPDB:GNC0028; CESP:CI7H11.6
A:Experimental source: strain Bristol N2; clone CI7H11
A:Gene: ICSP:CI7H11.6
A:Rep position: X
A:Introns: 47/3; 85/3; 122/3; 150/2; 187/2; 260/1; 331/1; 399/1; 448/1; 497/1; 534/3; 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 QPGKLRVQCGTCKQATLILAQGPSCWDDVLIPNRMSGECQSFDCPGTRAEFFFKCGAHFT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 OPGK----GKYKECPICAAKMPGS---AFP-KIKG-CQHRSCRACIRQY----- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 SDKDTSVALNLITSNRRSIPCIACTOVRSPVLVFQCNRRHVICLDGFHLYCVTRLNDRQF 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 VHDAQLGYSLPCVAGCPNSLIKELHHF---RILGEEQYTRYQQYGAZECVLQMGSVLCPR 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 -----IKMLIGDIPTLIEKYEAFSLRRYLMTEADARW-------CPA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 391 RVDKRAAEQARWEEASK----ETIKKTTKP-----CPRCNVPIEK--NGGCNHMKCPQPQ 439
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A; Reference number: Z20049
A; Accession: T25555
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Job time : 46 secs
                                         982 KREGCNHMQC---GCGTHYCWTC 1001
426 KNGGCMHMKCPQPQCKLEWCWNC 448
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RRP STOLENSE FROM N. A.

RRY SEQUENCE: FROM N. A.

RRY Adams N. D., Celliker S.E., Holt E.M., Hoskins R.A., Galle R.F.,

Adams C., Schere S.E., Holt E.M., Hoskins R.A., Galle R.F.,

A Adams N. C., Rogers Y. H.C., Diazol D., Chango O., Chanland C.K.,

RRY George R.A., Lowis S.E., Richards S., Ashburner M., Henderson S.N.,

RRY George R.A., Lowis S.E., Richards S., Ashburner M., Henderson S.N.,

Brandon R.C., Rogers Y.H.C., Diazol R.G., Champe M., Pécifére B.D.,

RRA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RRA Basia A., Baxendels C., Baytaktaroglu L., Bass.ey E.M.,

RRA Basia A., Basia A., Bandels C., Raytaktaroglu L., Bass.ey E.M.,

RRA Beson K.Y., Bonos P.V., Berman B.P., Branderi D., Bosshakov S.,

RRA Bericas K.C., Busam D.A., Buller H., Cadheu E., Center A., Chandra I.,

RRA Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,

RRA Cherry J.M., Cawley S., Dahlke C., Devenge M., Dugan-Rocha S.,

RRA Durkov E.C., Durn P., Durbin K.J., Evangelista C.C., Ferraz C.,

RRA Cherry M., Glasser M., Coup E., Downes M., Dugan-Rocha S.,

RRA Durkov E.C., Durn P., Loubin K.J., Evangelista C.C., Ferraz C.,

RRA Gebar W.M., Glasser M., Roller C., Gobortelian A.E., Garg N.S.,

RRA Gebar W.M., Glasser M.M., Rainsh F., Karpen G.C., Kraff C.,

RRA Gebar W.M., Glasser M.M., Rainsh F., Karpen G.C., Kraff C.,

RRA M.-H., Degawar C., Garain R.A., Martel B.E., Roiter C.D., Kraff C.,

RRA M.-La Z., Liang W.L. Moshrefi D., Merkulov G., Mishina M.V., Nobarry C.,

RRA M.-La Z., Liang W., Mesherson D., Merkulov G., Mishina M.V., Nobarry C.,

RRA M.-La Z., Liang W., Mesherson D., Merkulov G., Mishina M.V., Nobarry C.,

RRA M.-La Z., Liang W., Retchar R.A., Martel B.E., Roiter B., Rainshon M., Meskern D.R., Meskern 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A., CHARACTERIZATION, AND MUTAGENESIS.
STRAIN=Cregon-R;
MEDLINE=23341325; PubMed=10885484;
Aguilera M., Oliveros M., Martinez-Padron M., Barbas J.A., Ferrus A.,
"Axiadne-1: a vital Drosophila gene is required in development and
defines a new conserved family of ring-finger proteins.";
Genetics 155:1231-1244(2000).
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16-001-201 (Rel. 40, Last sequence update)
28-FEB-200 (Rel. 41, Last sequence update)
Ariadne-1 protech (Ari-1)
ARI-1 CR ARI OR CG5659.
Brosophila melanogaser (Fruit fly)
Brosophila melanogaser (Fruit fly)
Meoptora, Metazoa, Arthropoda, Hekapoda, Insecta, Pterygota,
Neoptora, Endoperygota, Diptera, Brachycera, Muscemorpha,
Ephydroidea, Erosophilidae, Erosophila.
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SEQUENCE FROM N.A.
  NCBI_TaxID=7227;
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29y4x5 homo sapien
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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         ----DSETSNW-----IAANTKECPRCSVTIEKDGG 303
                                                                                                                                                                                              Mile-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-200 (Rel. 41, Last amotation update)
48-Ris-BB-200 (Rel. 41, Last amotation update)
binding protein 1, (UbcH7-binding protein; (UbcM4-interacting protein)
77; Fragment)
Mile MRI OR WESH3PP CR UIP77.
Mile musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLIKE=20341325, Pubmed=10880484,
Aguilera M., Oliveros M., Martinez-Padron M., Barbas C.A., Ferrus A.,
Aguilera M., Oliveros M., Martinez-Padron M., Barbas C.A., Ferrus A.,
Akidane-1: a vital Drosophila gene is required in development and
defines a new conserved family of ring-finger proteins.?,
Genetics 155:1221-1244(2006)
-1- FINCTION: MIGHT ACT AS AN E3 UBIGUITIN-PROTEIN LIGASE, OR AS PART
OF THE B3 COMPLEX, WHICH ACCEPTS UBIGUITIN FROM SPECIFIC 22
USIGUITIN-COMPANIOS ENTYMES. SUCH AS UBEZI3/UBCM4, AND THEN
TRANSFERS IT TO SUBSTANTES.
                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordala, Craniata, Verlebrata, Euteleostomi,
Mammalia, Eutheria, Rodeniia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-198 FROM N.A.
STRAIN=CO-1, TISSUE=Embryo;
MEDLINE=99589765; Pubmed=10451816;
Artinnez-Noel G., Niedenhall R., Tamura I., Harbers K.;
A family of structurally related RING finger proteins interacts
specifically with the ubiquitin-conjugating enzyme UbcM4.";
FEBS Lett. 454:257-261(1995);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -: SUBCELJULAR LOCATION: MAINLY CYTOPLASMIC (BY SIMILARITY: TISSUE SPECIFICITY: Widely expressed. -: SIMILARITY: Contains 2 RING-type zinc fingers. -: SIMILARITY: Contains 3 IBR-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WGD, WGI:1344361, Arihi.
WGD, WGI:1344361, Arihi.
InterPro, IPROGESTI, Pribiquitin-dependent profein catabolism,
InterPro, IPROGESTI, Zh. G6HC.
InterPro, IPROGESTI, Zh. Zh. Zh.
SMART; SMOS447, IBR; 2.
SMART; SMOS447, IBR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE, PS00518, ZF_RING_1, FALSE_NEG.
PROSITE, PS50389, ZF_RING_2: 1,
Ubl conjugation pathway, Zinc-finger, Repeat, Coiled coil.
NCN TER
ZN_FING 97 146 RINS-TYPE 1.
ZN_FING 167 228 IBR-TYPE 2.
ZN_FING 255 300 RING-TYPE 2.
DOWAIN 97 165 INTERACTION WITH UBECLS.
                                             430 CMHMXCPQPQCKLEWCWNGGCEWNRACMGDHWFD 463
                                                                                304 CNHMVCKNONCKNEFCWVCLGSWEP--HGSSWYN 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF361001; AAX51471.1; -. EMBL; AC130977; CAA10275.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE OF 6-469 FROM N.A.
             268 KKWIKKCDD-----
                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10590,
                                                                                                                                                                       BSOCW
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                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the FMBL cutstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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RSP-RCH (ACIDIC).
RING-TYPE 2.
INTERACTION WITH UBCDIO.
COILED COIL (POTENTIAL).
C->Y: IN ARIL-2; LETHAL PHENCTYPE AND LOSS OF INTERACTION WITH UBCDIO.
C->Y: IN ARIL-3; LETHAL PHENOTYPE AND LOSS OF INTERACTION WITH UBCDIO.
C->Y: IN ARIL-3; LETHAL PHENOTYPE AND NO LOSS OF INTERACTION WITH UBCDIO.
C->Y: IN ARIL-3; LETHAL PHENOTYPE AND NO LOSS OF INTERACTION WITH UBCDIO.
                                                                                                                                                                                                                                      -!- SUBJUIT: INTERACTS WITH UBCDIO. CAN FORM DIMERS.
-!- SUBJUIT: INTERACTS WITH UBCDIO. CAN FORM DIMERS.
-!- SUBJUIT: INTERACTS WITH UBCDIVENSMIC.
-!- TISSUE SPECIFICITY: WIDELY BARRESSED, WITH PROMINENT LEVELS IN THE NERVOUS SYSTEM AND FEMALE GORADS.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN ALL TISSUES THROUGHOUT DEVELOPMENT, WITH MAXIMUM LEVELS REACHED DURING METAMORFHOSIS AND MAINTAINED IN THE ADULT.
-!- SIMILARITY: Contains 2 RING-type zinc finger.
-!- SIMILARITY: Contains 1 IBR-type zinc finger.
208 FFKCGAMPTSDKDTSVALNLITSNRRSIPCIACTOVRSP--VLVFQCNHRHVICLDCFHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00518; ZF RING : FALSE NEG-PROSITE; PS50089; ZF RING 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X98309; CAA66953.1; -. EMBL; X98310; CAA66954.1; -. EMBL; ABC03507; AAF4807.1; -. FlyBase; FB000017418; ari-1. InterPro; IPR001841; Znf_C6HC. InterPro; IPR01841; Znf_ring. Ffam; PF04485; IBR; 1. SMART; SMO0184; RING; 2.
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Matches 79; Conserv
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SEQUENCE OF 377-557 FROM N.A.
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Stanchi F., Bertocco
Cannata N., Zimbello
"Characterization of
                                                                  yeast seguences
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                                                                                                                                                                                                                                       monocytes."
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MIM; 60
    202 GTRAEFFFKCGAHPTSDKDTSVALNLITSNRRSIPCIACTDVRSPVLVF---QCNHRHVI 258
                                                                                                                                                                                           GNIEKLFAECHVINPSKKSRTRQMN-TRSSAQDMPCQICY-LMYPNSYFTGLECGHK--F 118
                                                                                                                                                                                                                                                                                                                                                172 LITNSFVECNRILKWCPAPDCHHVVVVQYPDAKPVRCK-----CGRQFCFNGGENWHDP 225
                                                                                                                                                                                                                                     259 CLDCFHLYCVTRLNDRQFVHDAQLGYSLFCVA-GCPNSLIKELHHFRILGEEQYTRYQCY 317
                                                                                                                                                                                                                                                                                                                        3.8 GABECVLOMGGVL--CPRPGCGAGLLPBQGQRK-VTCBGGNGLGCGFVFCRDCKEAYHE- 373
                                                                                                                                                                                                                                                                                                                                                                                                          374 ------GDCDSLLEPSGATSQAYRVDKRAAEQARWEEASKETIKKTTKPCPRCNVP 423
                                                                                                                                                                                                                                                                           119 CMCCWSEYLTTK-----IMEEGMGQTISCPAHGC-DILVDDNTVMRLITDSKVKLKYQH 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 VKCKWLKKWIKRCDD-------SETSNW----IAANTKECPKCHVT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C994\bar{XS}: O76026; O9H3T6; Q9UBNO; Q9UB39;
16-CCT-2031 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Ariadne-1 protein homolog (ARI-1) (Ubiquitin-conjugating enzyme E2-
binding protein 1) (UbcH7-binding protein) (UbcM4-interacting protein)
(HHARI; (H7-AP2) (HUSSY-27) (MOP-6).
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TISSUE-FECAL brain,
TISSUE-FECAL brain,
MEDLINE=9945297; FubMed=10521492;
Moynitan T.P., Ardley H.C., Nuber J., Rose S.A., Jones P.F.,
Markham A.F., Scheffner M., Robinson P.A.;
"The ubiquitin-conjugating eraymes UbcH7 and UbcH8 interact with RING
"The ubiquitins conjugating domains of HHARI and H7-AFI.";
J. Biol. Chem. 274:30963-30968(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 95-557 FRCM N.A. MEDLINE=20341325; PubMed=1089484; MEDLINE=20341325; PubMed=1089484; Aquilera N., Oliveros M., Martinez-Padron M., Barbas J.A., Ferrus A., "Aridane-1: a vital Drosophila gene is required in development and defines a new conserved family of ring-finger proteins.";
                                                                                                             Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                          . . . 9
                                                                  DB 1; Length 469;
                                                                                                          Indels
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  60 Y -> C (IN REF. 1).
55564 MW; 023EAD36333C7316 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.24 IEKNGGCMHMKCPQPQCKLEWCWNCGCEWNRACMGDHWFD 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 TEKOGGCNHMVCRNQNCKAEFCWVCLGPWEP--HGSAMYN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trockenbacher A., Marksteiner R., Schneider R.;
                                                              Query Match
9.2%; Score 237.5; DB J
Best Local Similarity 25.0%; Pred. No. 1.6e-11;
Matches 70; Conservative 43; Mismatches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished observations (MAY-2002)
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MEDLINE=21064499; PubMed=11124703;
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TISSUE=Brain;
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  CONFLICT
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use by non-profit institutions as long as its content is in me way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 CAVOMOFVRKENILSLACOHO -FORSCWECHCSVLVKD------GVÖVGTSCMAOROF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 KVTCEGGNGLGCGFVFCRDCKEAYH-EGDCDSLLEPSGATSCAYRVDKRAAEOARW---- 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 NSLIKELHHFRILGBEQYTRYQQYGABECV----LQMGGVLCPRPGCGAGL-1.PEQGQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 CIACIDV--RSPVINFOCNHRHVICLDOFHLYCVTRINDROFVHDAQLGYSJPCVA-GCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 LRTPEDFVFPLLPNEELROXYRRYLFRDYVBSHFQLQ--- LOPGADOFMVIRVQEPRAR
                                                                                                                                                                                                                                                                                                                                                                                                Zinc-finger;
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MEDLINE=99349709; Pubmed=10422847;
van der Reijden B.A., Erpelinck-Verschueren C.A.J., Loewenberg 5.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28C MUDICHANXISAHTKECPKCNICIEKNGGCNHNOCH-SKCKHDECMNCHCDMN 329
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Homo.
                                                                                                     R EMB3; AP124664; AA024573;;

R EMB1, AJ130975; CAA10273.1;

R MG7; MG7; MG7; AZ124.2;

R JINCEPPRO; 12803042; D. CGHC.

R INCEPPRO; 128031876; ZnCCGHC.

R INCEPPRO; 128031876; ZnCCGHC.

R Ffam, PP01465; IBR; ZnCCHC.

R SWART; SW0047; IBR; 2.

SWART; SW0047; ZnCCHC; 1.

R PROSITE; PS00184; ZnCCHC; 1.

R PROSITE; PS0189; ZnCCHC; 1
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1D ARIZ HUMAN

AC 095376; 090E26; 090E26)

DT 16-0CT-200: (Rel. 40, Last sequence update)

DT 15-SEE-2003 (Rel. 40, Last sequence update)

DT 15-SEE-2003 (Rel. 40, Last annocation update)

Mariadne-2 protein homolog (ARI-2) (Triadi protein) (HT005)

GN ARIH2 OR ARIZ OR TRIADI.
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COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
BSSEAS47EEG3ADAR CRC64;
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Mammalia, Butheria, Primates, Catarrhin, Hominidae,
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6.7%; Fred. No. 1.1e-10;
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52; Conservative
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2007
2007
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Best Local S
Matches 62
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TISSUE=Brain, and Embryo:
MEDIJINE=20314325; Pubmed=10880484;
MEDIJINE=20314325; Pubmed=10880484;
Aquillera M., Oliveros M., Martinez-Padron M., Barbas J.A., Ferrus A.;
"Ariadre-1: a vital Drosophila gene is required in development and defines a new conserved family of ring-finger proteins.";
Gene:cs 155:1231-1244(2030)
-!- FUNCTION: MIGHT ACT AS AN E3 UBIQUITIN-PROTEIN LIGASE, CR AS PART OF E3 COMPLEX, WHICH ACCEPTS UBIQUITIN FROM SPECIFIC E2 UBIQUITIN-CONJUBATING ENZYMES, SUCH AS UBE213/UBCM4, AND THEN TRANSFERS IT
                                                                                                                                                                                                                        GTRAEFFFKCGAHPTSDKDTSVALNLITSNRRSIPCIACTDVRSPVLVF---QCNHRHVI
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28-FEB-2003 (Rel. 41, Last annotation update)
Ariadne-2 protein homolog (ARI-2) (Triadi protein) (UbcM4-interacting
                                                                                                                                                                              Gaps
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                                                                                                                                                                              61;
237 D -> N (IN REF. 3).
303 F -> S (IN REF. 4).
316 ENWHDPVK -> AIGMILFO (IN REF. 4).
322 K -> T (IN REF. 4).
64118 MW, DFFF8965DAB41DC8 CRC64;
                                                                                                                                       Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/C; TISSUE=Liver;
MEDLINE=99358765; PubMed=10431818;
Martinez_Noel O., Niedenthal R., Tamura T., Harbers K.;
Ma family of structurally related RING finger proteins inter
specifically with the ubiquitin-conjugating enzyme UbcM4.";
FEBS Lett. 454:257-26;(1999).
                                                                                                                                   9.2%; Score 236.5; DB 1; Length 25.0%; Pred. No. 2.3e-11; tive 43; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEKNGGCMHMKCPQPQCKLEWCWNCGCEWNRACMGDHWFD 463
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ARIH2 OR ARI2 CR TRIADI OR UIP48.
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557 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RX MEDINE=2238855; Pubmed=12477932; RX MEDINE=2238855; Pubmed=12477932; RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Ratsster R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D., RA Alscebul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D., Halseh F., Cardar H., Moore T., Max S.I., Wang J., Halseh F., Esteleton M., Soares M.B., Banaldo M.F., Casavant T.L., Scheet T.E., RA Brownstein M., Gadres M.B., Banaldo M.F., Casavant T.L., Scheet T.E., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millary S.J. RA Raha S.S., McWan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Bosax S.A., McWan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., RA Richards S., Worley K.D., Soalergen E.J., Lu X., Gibbs R.A., Richards S., Worley K.D., Soalergen E.J., Lu X., Gibbs R.A., Raha J. Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Radiguez A.C., Grimwood J., Schmutz J., Dickson M.C., Sanchez A.M. Raha Schnerch A., Schein J.E., Jones S.J. M., Marra M.A., Gay L.C., Incorn M. Schein J.E., Jones S.J. M., Marra M.A., Thuman and cuse CDA sequences "I human and couse CDA sequences "I human and couse CDA sequences "I human and consecution and initial analysis of more than 15,002 full-length Thuman and consecution and initial analysis of more than 15,002 full-length Thuman and consecution and consecution and initial analysis of more than 15,002 full-congration confeasion and confeasion and consecution and 
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                                                                                                                                                                                                                                                    TISSUB-Hypochalamus,

WEDLINE=25402571; PubMed=1931946;

Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Fuang Q.-H., Ren S.-K.,

Gu Y.-C., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,

Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou C.,

Xu S.-H., Gu d., Shi J.-X., Jin W.-R., Zhang C.-X., Wu T.-M.,

Huang G.-Y., Chen M.-D., Chen J.-L.,

"Gene expression profiling in the human hypothalamus-pituitary-adrenal axis and full-length CDNA cloning."
MEDLINE=20341325; PubMed=10895484;
Aguilera M., Oliveros M., Martinez-Padron M., Barbas C.A., Ferrus A
Afaidene I.: a vital Drosophila gene is required in development and
defines a new conserved family of ring-finger proteins.";
Genetics 155:1211-1244(2000).
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-:- SUBCRILULAR LOCATION: Nuclear.
-:- SIMILARITY: CONTAINS 2 RING-type zinc fingers.
-:- SIMILARITY: Contains 1 IBR-type zinc finger.
-:- SIMILARITY: Contains 1 IBR-type zinc finger.
-:- CAUTION: REF.3 SEQUENCE DIPPERS PROM THAT SHOWN DUE TO
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GO:0005634; C:nucleus; TAS.
GO:0007275; P:development; TAS.
InterPro; IPR062867; Znf CEHC.
InterPro; IPR01878; Znf CEHC.
InterPro; IPR01841; Znf ZHO:0
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294 NSLIKELHHFRILGEEQYTRYQQYGAEECV----LQMGGVLCFRFGCGASL-LPEGGQR 347
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TISSUE-Fetal brain.
MEDINE-9925429; PubMed=10120776;
MEDINE-9925429; PubMed=10120776;
MENIN. SPAIN.
"Isolation and characterization of a novel human gene (HPB30) which encodes a protein with a FING finger motif";
prochim. Biophys. Acta 1445:232-236(1999).
SMART; SX00647; IBE; 2.
SMART; SX00184; RING; 2.
SMART: SX00343; ZDE C2440; 1.
PROSITE; PS00543; ZE ZNG 1; 1.
PROSITE; PS00699; ZF RING 1; 1.
PROSITE; PS00699; ZF RING 2; 2.
Ubl conjugation pattway: Ruchear protein; Goiled coll; 2:nc-finger:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 ADDSETANYISAHTKDCPKCNICIEKNGGCNHMQC--SKCKHDFGWMCLGPW 330
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Kammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo,
NCBI_TaxiD=1606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 --BEASKETIKKTIKPOPRONVPIEKNGGCMHMKCPQPQCKLEWCWNGGCEW 452
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TISSCENFERED brain;
MEDINE-990068094; PUDMOG=8851615;
UEKI N., Oda T., Kondo M., Yano K., Noguchi T., Muramaten M.-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.E%, Score 226, DB 1; Length 491; Best Local Similarity 26.7%; Pred. No. 1.3e-10; Matches 62; Conservative 33; Mismatches 81; Indels
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COLLED COIL (POTENTIAL).
CA -> LO (IN REF. 2).
30AFFED327ES1013 CRC64)
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Q9U3E38: 094793,
16-00T-201 [Rel. 40, Created)
16-00T-2001 (Rel. 40, Last sequence update)
15-SPP-2003 (Rel. 40, Last annotation update)
RING finger protein 14 (Androgen receptor-associated)
RING finger protein 14 (Androgen receptor-associated)
RN14_CR_ARA54;
                                                                                                                                                                                       ASP/GLU-RICH (ACIDIC)
POLY-GLU,
RING-TYPE 1.
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RING-TYPE 2.
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CONFLICT
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SEQUENCE FROM N.A. (ISSPECRM 1).

STRAIN-CSTBJ66; PubMed=11217618.

RA ARAWA T., Hara A., Subbara K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibara K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Subkunshi Y., Romo H., Adahi C., Pukuda S., Antawa K., Izawa M., Nishi K., Romo H., Romo S., Yamanaka I., Radota K., Okazaki Y., Osjobori K., Bono H., Kasukawa T., Salto R., Radota K., Matsuda H.A., Ashburner M., Bandlov S., Casavant T., Salto R., Radota K., Matsuda H.A., Ashburner M., Bold B., Rochiwa H., Radota K., Matsuda H.A., Salto R., Sizuki R., Tomita M., Ragner L., Washio T., Sha Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Ckido T., Furuno M., Ramina M., Wagner L., Washio T., Sakai K., Ckido T., Futcher C., Futcher C., Futcher C., Futcher C., Futcher C., Marina M., Lee N.H., Rashima M., Baldarelli S., Marinado M., But C., Schoenbach C., Nordiguez T., Sakanto M., Borocka K., Schoenbach C., Sakanto M., Soroki K., Schoenbach C., Shora M., Kawaji H., Kohisuki S., Winchaw Soris A., Voshida K., Wasegawa Y., Kawaji H., Kohisuki S., Kitoki Lona annocation of a fullilength mouse CDNA collection. W. Peter M. Peter M., Pater M., Matsuki S., Matsuki M., Teyocoka K., Wang K.H., Wettz C., Whittaker C., William B., Kitchional annocation of a fullilength mouse CDNA collection. W. Nature 409:635-630:2020.
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Van der Reljdem B.A., Jansen J.H.,
"Jenchilization of a novel TRIAD protein, TRIAD2.";
Submitted (MAR-2000) to the EMBL/GenBank/UDBU databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triad2 protein).
RNF14 OR ARAS4 OR TRIAD2.
Mus musculus (Mouse).
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                                                  -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
-!- TISSUE SPECIFICITY: Widely expressed.
-!- DOMAIN: THE N-TERMINAL DESTRUCTION BOX (D-BCX) ACTS AS A RECOGNITION SIGNAL FOR DEGRADATION VIA THE UBIQUITIN-PROTEASOME PATEWAY (BY SIMILARITY).
-!- DOMAIN: THE RING-TYPE ZINC FINSER IS ESSENTIAL FOR THE INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERACTION WITH ANDROGEN RECEPTOR.
C-SS: LOSS OF INTERACTION WITH UBEZEZ AND
C-AUTOUSIQUITINATION.
5.229EF5AF5BA5DAD CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Selection system for genes encoding nuclear-targeted proteins.";
Nat. Biotechnol. 16:1338-1342(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WITH UBEZEZ.
-!- PTM: RING-TYPE ZINC FINGER-DEPENDENT AND UBEZEZ-DEPENDENT AUTOUBLEQUITINATION.
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PROSITE; PS0518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Ligase; Ubl conjugation pathway; Transcription regulation;
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COILED COIL (POTENTIAL).
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-!- SIMILARITY: Contains 1 RING-type zinc finger.
-!- SIMILARITY: Contains 1 RWD domain.
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EMBL, AF060544, AADZ1842.1, -.
EMBL, AB015333, BAA34792.1, -.
Genew, HGNC110558, RNF14.
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350
395
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220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 RKVICEGGNGLGCGFVFCRDCKEAYH----BGBCBSLLEPSGAISQA------YRV 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----CIMGICSSCNFAFCTLCRLTYHGVSPCKVTABKLMDLRMBYLQADBANKRLLDQRY 379
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                                                                                                                                                       201 PGTRAEFFFKCGAHPTSD-----KDTSVALNLIT----SNRRSIPCI-----
                                                                                                                                                                                                                                        PNTELDFGGAAGSDVOQEEIVDERAVQDVESLSNLIQEILDFDQAQQIKCFNSKLFLCSI
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    Length 474;
                                                                           Indels
Query Match 8.7%; Score 223.5; DB 1; Best Local Similarity 26.0%; Pred. No. 2e-10; Matches 81; Conservative 34; Mismatches 123;
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RNÍ4_WCUSE STANDARD: PRT: 465 AA.
S9J30: Q9DCL2; Q9D6N2; Q9DSZ8; Q9J189:
16-0CT-2001 (Rel. 40. Created:
16-0CT-2001 (Rel. 40. Created:
16-0CT-2001 (Rel. 42. Last annotation update)
15-SEP-2003 (Rel. 42. Last annotation update)
RING finger proferin 14. Androgen receptor-associated protein

Bukaryota, Metazoa: Chordata; Craniata, Vortebrata, Euteleostomi, Marmalia; Eutheria: Rodentia; Sciurognathi: Muridae; Murinae; Mus

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240 CIDVRSPVLVFQCNHRHVICLDGFHLYCVTRIND--RQFVBDAQLGYSLPCVAGGEN--- 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -DSILEPSOATSQ--AYRVD 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 KRAJEQARWEEASKETIKKTIKPOPRONUFIEKNOGOMENKOFOPOCKJEWOWNOGOEWN 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 KRVIÇKALBEMBEKEMLEKNSKSOPCOGTPIOKLDGONKWIC--IGCMQYFOWICMSSLS 439
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MEDUTUE FROM N.A.
MEDUTUE FROM N.A.
MEDUTUE AGENCY STUDMED 10880484;
Aguilera M., Cliveros M., Martinez-Padron M., Barbas J.A., Ferrus A.
Aguilera M., Cliveros M., Martinez-Padron M., Barbas J.A., Ferrus A.
Aguilera M., Cliveros M., Martinez-Padron M., Barbas J.A., Ferrus A.
Gefines a new conserved family of ring-fingor proteins.";
Genetics 155:121-1244:2000!.
USAL -> GTLV (IN REF. 2: RAB26503/
BAB26741).
                                                                                                                                                                                                        55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      i6-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
Ariadne-2 protein (Ari-2).
ARI-2 OR ARIZ CR TRADI OR CGS709.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neopiera; Endonerygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                  Score 214; DS 1; Longth 46;
Pred: No. 1.2e-09;
***Mismatches 99; Indels
                                                                        C94307945B47112B CRC64;
                                                                                                                                   9.3%; Score 214; DS
Sest Local Similarity 27.2%; Pred. No. 1.2e
Matches 68; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 KVTCEGGNGLGCGFVFCRDCKBAYHE-GDC-
                                                                            485 AA; 54954 XW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                454 RACYGDHWFD 463
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          103
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      CONFLICT
                                                                        SECUENCE
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DR EMBL: AF24666: AAF7426.1;

EMBL: AF24666: AAF7426.1;

DR EMBL: AKC00783: BAB25541.1;

EMBL: AKC00783: BAB256741.1;

DR EMBL: AKC00162; BAB26741.1;

DR MGD: WG1: 129666: Raff.4.

DR GO: GO: GOS537: C: Cytcoplasm; ISS.

GO: GO: GOS537: C: Cytcoplasm; ISS.

GO: GO: GOS515: F: Picrotlation of transcription from Pol II pro. .; ISS.

GO: GO: GOS57: F: Experiment of transcription from Pol II pro. .; ISS.

GO: GO: GOS57: F: Picrotlation of transcription from Pol II pro. .; ISS.

GO: GO: GOS57: F: Picrotlation of transcription from Pol II pro. .; ISS.

THEEPPO: JER00657: RWD.

THEEPPO: JER00657: RWD.

THEEPPO: JER00657: RWD.

THEEPPO: JER00697: ZI _ GGHC.

SWART: SWO0691: RWD: 1.

FROSITE: PSSO089: ZF RING 1: 1.

THE DOMAIN AND ACTION PATHWAY: TRANSCRIPTION TEQUIATION;

DOMAIN ALLOS AND ACTION PATHWAY: TRANSCRIPTION TEQUIATION;

DOMAIN ALLOS AND ACTION PATHWAY: TRANSCRIPTION;

DOMAIN ALLOS AND ACTION PATHWAY: TRANSCRIPTION TEQUIATION;

DOMAIN ALLOS AND ACTION PATHWAY: TRANSCRIPTION;

FROM ALLOS AND ACTION PATHWAY: TRANSCRIPTION;

DOMAIN ALLOS AND ACTION PATHWAY: TRANSCRIPTION;

FROM ALLOS AND ACTION ACTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SÜBURIT: INTERACTS WITH THE UBIQUITIN-CONUJGATING ENZYMES UBEZEI AND UBEZEZ AND, IN THE PRESENCE OF TESTOSTERONE, WITH THE ANDROGEN ESCEPTOR (AR) (287 SIMILARITY).

SUBCEDIULAR LOCATION: Nuclear and cytoplasmic (By similarity).

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-ALA.
ASP/GLU-RICH (ACIDIC),
GNSNESLQNGSEYTICFLPPJVLNFEL -> ALCSLQAPR
QPVGRTPRQSGAVCLDAVS (in isoform 2).
FUNCTION: MIGHT ACT AS AN E3 UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS UBIQUITIN FROM SPECIFIC E2 UBIQUITIN-CONUGATING ENZYMES AND THEN TRANSFERS IT TO SUBSTRATES, WHICH COULD BE NUCLEAR PROTEINS. COULD PLAY A ROLE AS A COACTIVATOR FOR ANDROGEN AND, TO SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FIIG-VSP_005751.
Missing (in isoform 2).
/FIIG-VSp_005752.
V -> A (IN REF. 2).
G -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q9JI90-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RING-TYPE.
IBR-TYPE.
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ZN_FING
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405 ASKETIKKTTKPCPRCNVPIBRNGGOMHMKOPQPQCKLEWCWNGGOEW
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                                                                                                                                        STANDARD;
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                                                                              RESULT 9
YKZ7 YEAST
ID YKZ7 YEAST
P36113;
CUN199
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RA Wen W.-H., Ibegwam C., Jaiali M., Kalush F., Karpen G.H., Ke Z.,
Rayltz S., Kuip D., Lai Z., Lasko F., Lei Y., Levitsky A.A., Li C.,
Ra Mcavitz S., Kuip D., Lai Z., Lasko F., Lei Y., Levitsky A.A., Li C.,
Ra McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C.,
Ra McIris J., Moshrefi A., Mount S.M., Murphy B., Murphy L.,
Ra Misskern D.R., Pacleb J.M., Palazzolo M., Murphy B., Murphy L.,
Ra Muzny D.M., Nelson D.L., Nelson R.A., Nixon K.,
Ra Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S.,
Raplaton M., Strong R., Smen H., Shue B.C., Siden-Kiamos I.,
Rapleton M., Strong R., Smen H., Shen B.C., Siden-Kiamos I.,
Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R.,
Rapleton M., Strong R., Wang X., Wang Z.-Y., Wassarman D.A.,
Wenter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A.,
Ran Meinstock G.M., Weissenbach J., Williams S.M., Woodage T.,
Ran M., Zhou W., Zhou G., Zheng L., Zheng X.H., Zhong F.N.,
Ran M., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W.,
Rubin G.M., Venter J.C.,
Schence 287:2185-2195-(2000).
Cor El Complex MICH ACCEPTS UBIGUITIN-PROTEIN LIGASE, OR AS PART
CONJUGATING ENZYMES, SUCH AS UBCOILGINES IT RANSFERS IT
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CONTINES MENTAL MICH ACCEPTS UBIGUITIN PROM SPECIFIC E2 UBIGUITIN-
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CONTINES AND MARCH ACCEPTS UBIGUITIN MARCH 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 CNVRVPEDLVIIVTRPVMRD----KYQQFAFKDYVKSHPELRFCPGPNCQIIVQSSEIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 TPQYRSQMCPVCASSQLGDXFYSLACGHSFCKDCWTIYFETQIFQG---ISTQIGCMAQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104; Indels
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COLLED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNT: INTERACTS WITH UBCDIO.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Contains 2 RING-type zinc fingers.
-!- SIMILARITY: Contains 1 IBR-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASP/GLU-RICH (ACIDIC)
POLY-ALA.
RING-TYPE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. le-07; 33; Mismatches 10
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RING-TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.4%; Score 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01485; IBR; 1. SNART; SMO647; IBR; 2. P. PROSITE, PS00510; ZF RING 1: 1. PROSITE; PS50089; ZF RING 2: 1.
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Best Local Similarity
Local S9; Conservative
There 59; Conservative
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153
222
314
387
452
509 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 PEYTRLHYSPFVKCNSFHR...---FCFNCGFEVHSPADC--------KITTAW 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 KNDFTCIICCDKKDIBIFALECGHEY--CINCYRHYIKDKL-----HBGNIITCMDCSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEQGQRK----VTCEGGNGLGCGFVFCRDCK-FAYHEGDCDSLLEPSGATSQAYRVDKRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 AEQARWEBASKETIKKTIKPOPRONVPIBKNOGOMHMKGPQPÇCKLEWCWNGGCEWNRAC
                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast)
Eukaryota; Fungi, Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces,
NOSI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52:
                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2021 (Rel. 40, Last annotation update)
Hypothetical 63.6 kDa protein in YPTS2-GCN3 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.4%; Score 189; DB 1; Length B51; 4.0%; Pred. No. 1.3e-07;
102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duestoihoeft A., Moest D., Poenlmann R., Philipssen P., Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C044D520D228D618 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Contains 1 RING-type zinc finger.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 24.3%; Pred. No. 1.3e
nes 59; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RING-TYPE
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Page

us-09-830-703-4.rsp

protein). RNF19.

RN: 9 HUMAN

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361 FYFCRDCKBAYHEGD-ODSLLEFSGATSQAYRVDKRAABQARWERASKBTIKKTT-----414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BEFMURRWLVADPDC-----RWCPAPDCGYAVIAFGCASCP----KLTC---GREGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 SOKETSVALNLITSNRRS-----IPCIAC---TEVRSPVLVFQONHRHVICLEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 TÖKNSIFSTNTSSENGLISISKQIGDFIBÖPLGLLRHSKERFPD-IMTGHÄRS- CVOCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 HLY--------COVTRLNDRQFVHDAQ1GYSLPCVAGCPNSLIKELHHFRILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 RCYLRIBISESRVMISCPECTERFNP----HDIRLILS-------DDVLMEKY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESQYTRYQQYGABSCVLQMGGVLCPRPGCGAGI U. - . - . - PEGGQRKVT CEGGNGLGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----AARQERAQSIRIRIRSSSISYSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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PS0636; QSQUUS;

10-CCT-208 (Rel. 34, Croated)

16-CCT-201 (Rel. 40, Last annotation update

16-CCT-201 (Rel. 40, Last annotation update)

18-CCT-201 (Rel. 40, Last annota
                                                                                                                                                                                                                                                                                                                                                                                          -----KBCPRCNVPIBK--NGGGMHMKGFQPOCKLEWGWNG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jength 838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RING-TYPE.
Y -> H (IN REF. 3 AND 4).
S -> R (IN REF. 4; CAB53700);
7 15BD616A52256336 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.2%; Scare 184.5; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 4.9e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29; Mismatches
248 TEFCYHCKOIWHPNQTCD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     838 AA; 90722 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Stmilarity 24.2%
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----- EWNR 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLUAR LOCATION: EXPRESSED PRIMARILY IN THE XY BCDY OF PACHYTENE SPERMATOCYTES AND IN THE CENTROSCME OF SOMATIC AND SERM CELLS IN ALL PHASES OF THE CELL CYCLE.

TISSUE SPECIFICITY: WIDELY EXPRESSED AT LOW LEVELS MITH HIGH LEVELS FOOND IN THE HEART. UBIGUITOUSLY EXPRESSED IN THE CENTRAL NERVOUS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Spinal cord;

BEDL'ARB-2113402; PubMad=11237715;

Niwa 7.11, Tanaka K., Sobue G.;

"A novel centrosomal ring-finger protein, dorfin, mediates ubiquitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Hepatoma, Ovarian carcinoma, and placenta;

TISSUE-Hepatoma, Ovarian carcinoma, and placenta;

TISSUE-Hepatoma, Ovarian carcinoma, and placenta;

TISSUE-Hepatoma, Varian carcinoma, T., Cisuki T., Suzuki Y.,

Tanai H., Kimata M., Wakamabe M., Hiraoka S., Ishii S., Kawai Y.,

Saito K., Yamamoto J., Wakamatsu A., Nakamira Y., Nagahari K.,

Masuho Y., Kanehori K., Kawabata A., Hikli T., Chotake N.,

Inagaki H., Ikema Y., Okamoto S., Okitani R., Obayasin M., Nishi T.,

Shibahara T., Tanaka T., Takahashi-Fujii A., Hara H., Tanase T.,

Nabekura T., Oshima A., Hara R., Takeuchi K., Arita M.,

"NEDO human cona sequencing project.";

Submitted (FEB-2000) to the EMEL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., FUNCTION, SUBCELLUDAR LOCATION, AND TISSUE
SPECIFICITY.
                                                                                                                                                       RN19 HUXAN STANDARD, PRT, 838 AA.
09NV58: CH5H9; C9H8X8: QUUFG; C9UFX6: Q9Y4X1;
16-OCT-20C: (Rel. 40, Created)
16-OCT-20C: (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RING finger protein 19 (Dorfin) (Double ring-finger protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gunther M., Laithler M., Brison G.;
A set of proteins interacting with transcription factor Spl
identified in a two-hybrid screening.";
Mol. Cell. Blochem. 210:131-142(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 422-824 FROM N.A., AND INTERACTION WITH SPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 18R-type zinc finger.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 281:706-713(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20431278; PubMed=10976765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 142-838 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 524-838 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity.";
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360 247

367 233

24.3

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Broinformatics and the BMED distracts the Bussel Brone by the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseaisb-sib.ch.
                                                                                                                                                                                                290 ESGAAADDIKPOPRCAAYIIKANDGSCNBMTO--AVGGCEFGWLCMKEISDLHYLSPSGC 347
160 RQYLRIEISESRVNISCPECTERFNP----HDIRLILS-------DDVLMEKY----- 201
                                             308 BEQYTRYQQYGAEECVLQMGGVLCPRPGCGAGLL-----PEQGQRKVTCEGGNGLGCG 360
                                                                                                                                      248 TEFCYHCKÇIWHPNÇTCD-------ARQERRGSLRIRTIRSSSISYSÇ 289
                                                                          202 BEPYLRRWLVADPDC-----RWCPAPDCGYAVIAFGCASCP----KLTC---GREGOG
                                                                                                         361 FVFCROCKBAYHEGD-CDSLLEPSGATSQAYRVOKRAABQARWEBASKETIKKTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryoča, Medazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Cafarrhini: Hominidae, Homo.
NOBI TaxiD=5506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cuery March

8.3%: Score 162.3: DB 1: Length 292:

Rest Local Similarity 24.6%: Pred. No. 9.3e-06;

Matches 62; Conservative 36; Mismatches 91; Indels 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415 -----KPCPRCNVPISK--NGGCMMKCPQPQCKLEWCWNG
                                                                                                                                                                                                                                                                                                                                                               01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
28-FES-2033 (Rel. 41, Last annotation update)
JUDGUIDIN CONJUGATING ENZYME 7 INTERACTING protein 4
Inherracting procesh 4) (RNG finger protein 144).
EMP144 OR UBGSTIP4 OR KIAROLA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBE, D79983; BAA11478.1; -.
                                                                                                                                                                                                                                                                                                                                       STANDARD
                                                                                                                                                                                                                                 -----EWNR 454
                                                                                                                                                                                                                                                              348 TPWGKKPWSK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       UTI4 HUMAN
PBC376;
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                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EXBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 SDKDTSVALNLITSNRRS-----IPCIAC----TDVRSPVLVFQCNHRHVICLDCF 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 ADKNSIFSTNISSENGLISISKQIGEFIECPLCLLRHSKDRFFD-IMICHHRS--CVDCL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 HLY-------CVTRINDRQFVHDAQLGYSIPCVAGCPNSLIKELHHFRILG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains : IBR-type zinc finger.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
-!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 778
ONWARD DUE TO A FRAMESHIFT.
                                                           Parraga M., del Mazo J.;
"XYBD, a novel RING-finger protein, is a component of the XY body of
Spermatocytes and centrosomes.";
Mech. Dev. 90:95-10:12005:
                                                                                                                                                        STRAIN=CD-:,
MEDLINE=99158765; PubMed=10431818;
MEDLINE=99158765; PubMed=10431818;
Martinez-Noel G., Niedenchal R., Tamura T., Harbers K.;
"A family of structurally related RING finger proceins interacts
specifically with the ubiquitin-conjugating enzyme Jocx4.";
FEBS Lett. 4541257-261(1999):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.2%; Score 184.5; DB 1; Length 840; Best Local Similarity 24.2%; Pred. No. 4.9e-07; Matches 75; Conservative 28; Mismatches 80; Indels 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RING-TYPE,
HAC117A35849C023A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ubl conjugation pathway; Zinc-finger; Metal-binding ZN_FING 52 117
           SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
STRAIN=Swiss; TISSUE=Testis;
MEDLINE=20054096; Pubmed=10585566;
                                                                                                                       [2] SEQUENCE OF 97-245 FROM N.A., AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSOCS18; ZF_RING 1; FALSE_NEG.
PROSITE; PSSOC89; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF120207, AAF18303.1;

EMBL, AF120206, AAF18302.1;

EMBL, AF301560, AAG37798.1;

EMBL, AF30099, AAK3169.1;

EMBL, X71642; CAA50643.1; ALT_FRAME.

MGD; MGI:1353623; Rnf19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR0C2867; Znf_C69C.
InterPro; IPR001841; Znf_ring.
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Pfam, PF03097; zf-C3HC4; 1.
SMART; SM00647; IBR; 2.
SMART; SM00184; RING; 1.
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                                                                                                                                    328 GVICPRPGCGA-----GLIDPEGGRKVTCBGGNGLGCGFVFCRDCKEAYHEGD-CDSL 379
                                                                                                                                                                                                        380 LEPS---GATSQAYRVDKRAAEQARWEEASKETIKKTTKPCPRCNVFIEKNGGCMHMKCP-434
                                                                                                                                                                                                                             160 MPITFLEGETSAAFKXEEDDA-------PIKRCPKCKVYIERDEGGAGMMC- 203
                                                                                               49 QYV-ELLIKEGLETAISCPDAACPKQGHLQENEIECHVAAEIMQRYKKLQFERBVLFDPC 107
215 PTSDKOTSVALNLITSNRRSIPGIACTDVRSPVLVFGCNHRHVICLDCFHLYCVTRLNOR 274
                                                              275 QFVHDAQLGYSLPCVAGCPNSLIKELHHFR-----ILGBEQYTRYQQYGAE-BCVLQMG 327
                             8 PTWD----LALDPLVSCKL---CLGSYPVECMTTIAQCQ-----CIFC--TLCL----K 48
                                                                                                                                                                    RIWCPASTCOAVCQLODVGL---OTPOPVQCK----ACRMEFCSTCKASWHPGGGCPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazca, Chordata; Craniata, Vertebzata; Buteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
17-SEP-2003 (Rel. 42, Rang England Protein 4)
18-SEP-44 OR UBCETIP4 OR UIP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Martinez-Noel G., Pringa E., Harbers K.,
Submitted (MAR-2001) to the EMBL/GenBank/DOBC databases.
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SEQUENCE FROM N.A.
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SECURANDE FROM N.A.

SECURAL FROM N.A.

SCHOOLS FALL N. Grouse L.H., Derge J.G.,

RA Klausner R.D., COLING F.S., Wagner L., Schooler C.M., Schuler G.D.,

RA Altschul S.P., Zeebrer F.S., Wagner L., Schooler C.K., State N.K.,

RA Altschul S.P., Jordan H., Moore T., Max S.I., Wang J., Hatch F.,

RA Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci F., Prange C.,

RA State S.S., Jordan H.S., Toshiyuki S., Carninci F., Prange C.,

RA State S.S., Jordan M.S., Peters G.J., Abramson R.D., Millaby S.C.,

RA State S.S., Jordan H.J., McKernan K.G., Malek J.A., Gibbs R.A.,

R. Charlon D. M., Wardy M.C., Haje S., Garcia A.M., Gay D.J., Hulyk S.W.,

R. A. Thilaco D. K., Wizny D.M., Sodergree E.J., Ju X., Gibbs S.A.,

R. A. Halton E., Ketteran V.C., Shevchenko Y., Bouffard G.G.,

R. A. Halton E., Ketteran C.C., Shevchenko Y., Bouffard G.G.,

R. A. Bakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

R. A. Butterfield V.S.N., Krzywinsk M.L., Skalska U., Smallus D.E.,

R. Butterfield V.S.N., Krzywinsk M.L., Skalska U., Smallus D.E.,

R. Butterfield V.S.N., Krzywinsk S.C.M., Maxra M.A.,

R. Human and mouse colk sequences "., Mose than 15,000 full-length

R. "Cherzdular Location Nuclear By similarity).

C. -- SUBCELJULAR LOCATION: Nuclear B.D. Similarity).

C. -- SUBCELJULAR LOCATION: Nuclear B.D. Similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 RSIPCIACTDVRSPVLVFQCNHRHVICLDCFHLYCVTRINDRQFVHDAGLGYSLPCVAGC 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66. FDAACPKQGHLQBNEIBOMVAABIMQRYKKLQPERBVLFDPCRTWCPASTOQAVCQLQDI. 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLIPEQGQRKVTCEGGNGLGCGFVFCROCKEAYHEGD-CDSLLEPS---GATSQAYRVDK 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SI:--- QIPQLVQCK----- ACDMEFCSACKARWHPGQGGPEIMPITFLPGEISSAFKMER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 86
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Local Similarity 22.4%; Pred. No. 1.6e-05;
Hes 65; Conservative 36; Mismarhan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AF360996, AAK51468.1) -- EEMBL, AK038086, BAC30088.2, -- EMBL, BCC30087, AAE30167.1, -- KG3, MG11244401, RNÉ144.
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RESULT 14 YMG8 YEAST

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT endry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics, and the EMBS outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nitted (SEP-2002) to the EMBL/GenBank/DCBJ databases.
STOCTION: MIGHT ACT AS AM ED UBLOUTTN-PROFILIN LIGASE. OR AS PART OF ED COMPLEX, WHICH ACCEPTS UBLOUTIN'S FROM SPECIFIC ED UBLOUTING PROM SPECIFIC ED UBLOUTING CONJUGATING ENZYMES, SUCH AS UBC-2/URB213, AND THEN TRANSFERS IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 RABFFEKC--GAHPTSDKDTSVALNLITSNRRSIPCIACT-DVRSPVLVPQCNHRHVICL
                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
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PROSITE; PS00218; ZF RING_1; FALSE_NEG.
PROSITE: PSSC089; ZF NING_2; FALSE_NEG.
Ubl conjugation path#ay; Nuclear protein; Colled coil; Zinc finger;
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the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                   i.6-ocr-2001 (Rel. 40, Created)
28-FB3-2003 (Rel. 41, last sequence update)
28-FB3-2003 (Rel. 41, last annotation update)
Probable ariadne-2 protein (Ari-2).
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WormPep; T12812.1; CE31725.
InterPro; PR002967; Znf_C6HC.
InterPro; IPR001947; Znf_xing.
Pfan; PF01463; ISR; 2.
SMART; SXC647; IBR; 2.
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STRAIN=Bristol N2,
Bradshaw H., Stellyes E.
Submitted (JUL-1996) to
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nes 58; Conserv
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Waterston R.;
Submitted (SEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----HHFRILGEEQYTRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEQ-GQRKVTCEGG 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---KCHFVFCFDCLHAWHGYNNKCGKKVSLSTDIIEEYLDDIVTSYERKREE-AKYGRR 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 KCGAHPISD -- KDISVALNLIISNRRSIPCIACIDVRSPVLVFQ-----CNHRHVICLDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 KCLIQDQYDLFKQISEBATLQKVSRSNYHCCICMEMEKGVRMIKLPCENANVEHYLCRGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 AKSYFTAMIQENRISSVRCPQCEYKELKLEDFKSYKKMLKALFTP11---PVSFLKEVID
                                                                                                                                                                                                                                                                                                                                                         Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.:
"The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII."
                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIRST 548329; S48328.
SGD; S0004533; YML068W.
SGD; S0004533; YML068W.
SGD; G0:005649; P:regulation of translational termination; IMP.
InterPro; IPR02867; 2nf C6HC.
InterPro; IPR01841; Znf Ting.
Pfam; PP01485; IBR; 2.
SWART; SW00647; IBR; 2.
SWART; SW00647; IBR; 2.
PROSITE; PS0C518; ZF RING; 2.
PROSITE; PS0C518; ZF RING; 2.
PROSITE; PS0C689; ZF RING; 2.
Hypothetical protein; Zing-finger.
ZN_FING
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                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical 54.1 kDa protein in DAKI-ORC1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.6%; Score 144; DB 1; Length 464
22.6%; Pred. No. 0.00041;
ative 34; Mismatches 119; Indels
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     464 AA
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Best Local Similarity 22.65
Matches 68, Conservative
  STANDARD;
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                                                                                                                                                                                                                                                                                                                                 STRAIN=S288c / AB972;
PubMed=9169872;
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YMG8_YEAST
Q04638;
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5.1.6 Compugen lad.	ch time 100 seconds	000 million cell updates/sec 000 million cell updates/sec 000 million cell updates/sec			3: 830525						predicted by chance to have a score of the result being printed, total score distribution.		Description	O9wvs6 mus musculu Q9jm64 rattus norv O9jk66 rattus norv	Q8K506 rattus norv Q93111 rattus norv	Q8k5c3 rattus norv Q8k5c5 rattus norv	060260 homo sapien QBww07 homo sapien	Ogni44 homo sapien Ogni44 homo sapien Oges22 mus musculu	O9es23 mus musculu O95ti4 drosophila	Q9vp72 drosophila Q8k5c4 rattus norv
GenCore version 5.1 Copyright (c) 1993 - 2002 Compu	Otein search, using sw model October 21, 2503, 21:23:49 , Search	1197.33 US-09-830-703-4 2573 1 MIVEYRENSSYGEPUBVDSD	ın	830525 seqs, 258052604 residues	hits satisfying chosen parameters	length: 0 length: 2000000000	<pre>. Minimum Match 0% Maximum Match 100% Listing first 45 summaries</pre>	SPTREMBL 23:* 1: Sp_archea:* 2: Sp_bacteria:* 3: Sp_fungi:* 5: Sp_invertebrate:* 6: Sp_mammal:*			a pre	SUMMARIES	uery atch Length DB	100.0 464 11 09MVS6 95.7 465 11 09GM64 95.5 465 11 09GK66	489 11	437 11	387 4	274	262 11	482 5 203 11
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DT 01.NOV-1999 (TFEMBURE): 12, Created)
DT 01.NOV-1999 (TFEMBURE): 12, Last sequence update)
DR 01.NOV-1999 (TFEMBURE): 12, Last sequence update)
DR 01.NOS-1999 (TFEMBURE): 12, Last sequence update)
DR 01.NOS-1999 (TFEMBURE): 12, Last sequence update)
DR 02.LastDates: Novel 12, Last sequence update)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murimae, Rattus.
                                                                                                                             Gaps
                                                                                            DB 11; Length 465;
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                                                                                      95.7%; Score 2458.5; DB 11; Lengt
94.8%; Pred. No. 3.6e-223;
iive 11; Mismatches 12; Indels
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EMBL; AF257234; AAF68666.1; -.
EMBL; AF210434; AAG37013.1; -.
 SMART: SX00213; UBQ; 1.
PROSTTE; PEDD129; THID: PROTEASE CYS; 1.
PROSTTE; PEST063; UBIQUIN 2; 1.
SEQUENCE 465 AA: 51678 NW; ADA8843EC69A487A CRC64;
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Last annotation update)
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"Molecular cloning of rat Parkin gene.";
Submitted (APR-2000) to the EMBL/GenBark/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9JX66 PRELIMINARY; PRI,
C9JX66;
01-0CT-2000 (TEBMELTEL, 15, Created)
01-0CT-2000 (TEBMELTEL, 15, Last sequel-C1-YAR-2003 (TEBMELTEL, 23, Last anno
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STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
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InterPro: IPRC03977; parkin.
InterPro: IPRC0169; SHpror_acsite.
InterPro: IPRC0626; Ubiquiin.
InterPro: IPRC0626; Ubiquiin.
                                                                                                          il Similarity 94.8
441; Conservative
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TISSUE-Hypothalarus;
Gu W.J., Abbas N.E.;
"Rat Parkin CDNA.";
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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                                                                                        100.0%; Score 2570; DB 11; Length 464; 100.0%; Pred. No. 1.1e-233; ive 0; Mismatches 0; Indels 0;
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Hattori N., Wang M., Mizunc Y.;
"The expression of parkin mRNA in developing, adult and
CNS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2000) to the EMEL/GenBank/DDBJ databases EMBL; ABC39878; BAA92431.1; ...
HSSP; P02248; 1UBI.
SMART; SM00213; UBQ; 1.
PROSITE; PS00139; THIOL PROTEASE CYS; 1.
PROSITE: PS50053; UBICUIT:N 2; 1.
SEQUENCE 464 AA; 51617 XW; 5574A285A9A1B09G CRC64;
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InterPro; 1PR00169; SHprot_acsite.
InterPro; 1PR000626; Ubsquitin.
InterPro; 1PR00286; Ubsquitin.
Pfam: PF01485; 1BR; 1.
Pfam: PF0240; ubsquitin; 1.
PRINTS; PR01475; PRNIN.
PRINTS; PR0344; UBRSIN.
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(TrEMBirel, 15, I
(TrEMBirel, 23, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGAGLLPEQGORKYTCEGGNGLGCGFVFCRDCKEAYHBGDCDGLLEPSGAJSQAYRVDKR 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAEQAKWEEASKEIIKKTTKPOPRONVPIEKNGGOMHMKOPOPQCKLEWOWNGGOEWNRA 455
                                                                                                                                                                                                                             \Theta
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                                                                                                                                                                                             1 MIVEVRENSSYGEPVEVESDISILQLKEVVAKEQGWPADQURVIFAGKEDFNHLIV----
                                                                                                                                                                                                                181 VQPGKURVQCGTCRQATUTLAQGPSCWDDVLIPWRMSGECQSPDCPGTRASPPFKCGAHP
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkin (Fragment).
Ratus norvegicus (Rat).
Eukaryota, Matazoa, Chordata: Craniata, Vertebrata, Euteleostomi)
Mammalia: Eutheria, Rodentia: Schurognaffil, Muridae; Murinae; Rat
NGST_TaxiD=10116:
                                                                                                                                                    22.5
                                                                                                             DB 11; Length
                                                                                                         94.7%; Score 2433.5; DB 11; Length
90.0%; Fred. No. 8.8e-221;
11vc - 12; Mismatches - 12; Indels
        SYART; SMC0213; UBC; 1.
PROSITE; PS00139; TH:01 PROTEASE CYS; 1.
PROSITE; PS50053; UBLCUTIN 2: 1.
SEQUENCE 489 AA: 54417 YM; 49F53B8F3E82ABS CRC64;
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X MEDINE-2015372: PubMed=10686159;

A Cloning and distribution of the rat parkin mRNA.";

Brain Res. Mol. Brain Res. 75:345-349(2000).

R BREL AF.68004; AAF34874.1;

R BREL AF.68004; AAF34874.1;

R InterPro; IPR00169; SHprot acsite.

R InterPro; IPR00169; Shprot acsite.

R InterPro; IPR002667; Ubiquitin.

R InterPro; IPR002667; Znf_C6HC.

R Pfar; PF01485; IBR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9JLL: PRELIMINARY, FRT, 455 AM.
Q9JLL:
C1-CCT-2000 (TrEWELrel. 15, Created)
C1-CCT-2000 (TrEWELrel. 15, Last sequence update)
C1-MAR-2003 (TrEWELrel. 23, Last annotation update)
                                                                                                           Query Match
Best Local Similarity 90.03
Matches 440; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CMGCHWFDV 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                456 CMGDHWFDV 464
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                                                                                                                                                                                                                                                                                                                                                                                              121 VILDTDSKRDSEARRGP-VKPTYNSF1YCKGPCHKVQPGKLRVQCGTCKQATLTLAGGP 179 [[[[[[[]]]]]]] [[[[]]]] [[[]]] [[[]]]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIDVRSPVLVFQCNHRHVICLDCFHLYCVTRLNDRQFVHJAQLGYSLPCVAGCPNSLIKE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEVEGRÖCKRAYHEGDCDSLLEPSGATSGAYRVDKRAAEQARWEEASKETIKKTTKR20R 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MIVEVARENSSYGEPVEVDSDISILOSKEVVAKRQGVPADQLEVIFAGKELPNHLIVQNOD 60
                                                                                                                                                                                                                                                                                                                     1 MIVEVRENSSYGFPVEVDSSTSIFQLKEVVAKRQSVFADQLRVIFAGKELDNHLTVQNCF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-007-2002 (TrEMBLrel. 22, Created)
01-007-2002 (TrEMBLrel. 22, Last sequence update)
01-08-2002 (TrEMBLrel. 23, Last annotation update)
Parkin isoform.
Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBL TaxID=10116,
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                            Query Match 95.5%; Score 2455.5; CB 11; Length 465; Best Local Similarity 94.6%; Pred. No. 7e-223; Matches 440; Conservative 12; Mismatches 12; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANINSEPROGREDANIEY;
D'Agara V., Scapadnini S., Cavallaro S.,
D'Agara V., Scapadnini S., Cavallaro S.,
I "Functional and molecular diversity of parkin.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AF391277; AAM21452.1;
R InterPro; IPR003977; parkin.
R InterPro; IPR001695; Siprot acsite.
R InterPro; IPR001695; Siprot acsite.
R InterPro; IPR001695; Siprot acsite.
R InterPro; IPR01695; IBR: 1.
R PRINTS; PR01485; IBR: 1.
R PRINTS; PR01475; PARKIN.
SWART; SY00647; IBR: 2.
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Pfam; PF01485; IBR; 1.
Pfam; PF00240; ubiquitin; 1.
PRINTS; PR01475; PARKIN.
SMART; SM0647; IBR; 2.
SMART; SM00213; UBC; 1.
PROSITE; PS00139; IHIOL PROTEASE CYS; 1.
PROSITE; PS00139; UBC; 1.
PROSITE; PS00139; UBC; 1.
SEQUENCE 465 AA; 51708 NF; BI3CF170Ab60242B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNVPIEKNGGCMHMKCPQPQCKLEWCWNCGCEWNRACMGDHWFDV
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                                                                                                                                                                                                                                                                                611
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                                                                                                                                                                                                                                                                                                                                                                  180 SCWDDVLIFNRMSGEOGRPBOPGTRAEFPFKCOAHPTSDKBTSVALKLITSNRRSIFGLA 239
                                                                                                                                                                                                                                                                                                                                                                                         SCWDDVLIPWAMSGECOSPHOPGISAEFFFKOGAHFISCKEIPVALHLIATMSRNITCIT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THHFRILGEBQYTRYQQYGAEECVLCMGGVLCPRPGCGAGLLPEQGGRKVTCEGGNGLGC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEVECROCKEAYHEGDCDSLLEPSGATSQAYRVDKRAAEQARNEEASKETIKKTTKFCPR 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEQUSIVHIVORPRARSHETNASGGDEPQSTSEGSIWESRSLITRVDLSSHTLFVDSVGLA 120
                                                                                                         L MIVEYRENSSYGEPVEVDSDTSILQIKEVVAKROGVPAGQLRVIFAGKELPNHUTVQNCD 60
                                                                                                                                                    60
                                                                                                                                                1 MIVEVRANSSHOFPVEVDSDISIFQLKEVVAKRÇGVPADQLRVIFAGKBLRNDWIVÇNCD
                                                                                                                                                                                                                                                                                121 VILDIDSKRDSEAARGEV-KPTYNSFFIYCKGPCHKVQEGKLRVQCGTCKQAILILAQGE
                                                                                                                                                                                                                                                                                                         121 VILHIDSRKDSPRAGSFAGREIYNSRYYCKGRÇORVQRGKLRYQOSICROAILILIQOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTDVRSPVLVFOCNHRHVICLDCFHLYCVTRLNDRQFVHDAQLGYSLPCVAGCPNSLIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIDVRSPVLVFOCNSRHVICLDCFHLYCVIRLXDRQFVHDFQLGYSLFCVAGCPNSLIKE
                                                                Gaps
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
02-Marian to Parkinson disease (Autosomal recessive, juvenile) 2,
03-Maryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleosioni,
03-Mammalia, Euthersa, Primates, Catarrhini, Homindae, Horo.
                                                             .;
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                      DB 4) Length 465;
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79.0%; Pred. No. 18-142;
IIVe 21; Mismatches 39; Indels 2
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Suranskeng R.,

Submitted (JAM-2002) to the EMBL/GenBank/DDBL databases.

RMBL, BCD22014; AAH22014::

R TherPro; IPRO03897; Darkin.

INTERPO; IPRO0626; Ubguitin.

INTERPO; IPRO0689; Zf-Sec24.

R FAm; PF0046; TBR; 1

R FAm; PF0046; Ubguitin.

R PAm; PF0046; Ubguitin.

R PRINTS; PRO046; Ubguitin.
                                                             Indels
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1 42407 MW, 4800F41086226506 IND64;
                                           le-196;
s 47;
                    Query Match

84.5%; Score 2170.5;

Best Local Similarity 83.4%; Pred. No. 5.1e-
Matches 369; Conservative 29: Mismatches
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Best Local Similarity
Matches 301, Conserv
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                                                                                                                                                                           61 LEQQSIVHIVÇRPQRKSHBINASGGDKPQSTPEGSIMEPRSLIRVDLSSHILPADSVGLA 130
                                                                                                                                                                                                                                                                                                                    SCWDDVLIPNRMSGECQSPDCPGTRAEFFFKCGAHPTSDKDTSVALNLITSNRRSIFCIA 239
                                                                                                                                                                                                                                                                                                                                                                                                                             300 LHHFRILGEEQYTRYQQYGABECVLQMGGVLCPRPGCGAGLLPEQGCRKVTCEGGNGLGC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MIVEVRENSSYGEPVEVDSDISILOLKEVVAKROGVFADOLRVIFAGKELPNHLIVGNCD 60
                                                                                                      69
                                                                                    VILDITESKRESEAARGP-VKPTYNSFFTYCKGPCHKVQPGKLRVQCGTCKCATLTLAGGP
                      Gaps
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Mammalia, Eutheria, Primates, Catarthini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE=9819084; PubMed=9560156; Kitada T., Yamatura Y., Kitada T., Yokawa S., Hattori N., Matsumine H., Yamatura Y., Minoshima S., Yokochi M., Mizuno Y., Shimizu N.; "Mutations in the parkin gene causes autosomal recessive juvenile
                    14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS, PRO1975; PARKIN.
PRINTS, PR00348; UBIQUITIN.
SWART; SW00647; IBR; 2.
SWART; SW00213; JBQ; 1.
PROSTIE; PS0019; THIOL PROTEASE CYS; 1.
PROSTIE; PS00053; UBIQUITIN. 2; 1.
SEQUENCE 465 AA; 51650 NM; 6A9BB99B876ECCAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created:
Last sequence update:
Last annotation update:
93.1%; Pred. No. 4.2e-199;
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                    14; Mismatches
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Interbro: IPR00397; parkin.
Interbro: IPR003097; parkin.
Interpro: IPR000626; Ublquitin.
Interpro: IPR000626; Ublquitin.
PGam; PP00485; IBR; 1.
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060260,
01-AUG-1998 (TREMBLE1, 07,
01-AUG-1998 (TREMBLE1, 07,
01-NAR-2003 (TEMBLE1, 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parkinsonism.";
Nature 322.605-608(1998).
EMBL; AB009973; BAA25751.1;
HSSP; PG2248; IUBL.
                      405; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Humar)
Best Local Similarity
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                  Matches
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371 YHEGDCDSLLEPSGATSQAYRVDKRAAEQARWERASKETIKKTTKPCPRCNVPIEKNGGC 430
                                                                                                     QONHRHVICEDCFHEYOVTRENDRQFVHDAQEGYSLPOVAGOPNSEIKELHHFRILGEEQ 120
                           YTRYQQYGAEECVLQMGGVLCPRPGCGAGLJPEQGQRKVTGEGGGGFVFCRECKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE, PS00139, THIOL PROTEASE CYS, 1.
SEQUENCE 274 AA: 30626 MW; JĀRSD26C14AB17CC CRC64;
                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.3%; Score 1420; DB 4; 88.3%; Pred. No. 1.5e-125; Ive 13; Mismatches 19;
                                                                                                                                            431 MAMKOROPOCKLEWOWNOGOEWNRACMGDRWFUV 464
                                                                                                                                                             MENKAPOPOCKEBWCWNGGGBWRRACMGCHWFDU 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 MEMKOPQPQOKLEWOWNCGOEWNRACMGDHWFDV 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEMICEPOPOCALEWOWNOGOBWIRVONGDEWFOV
                                                                                                                                                                                                                                                                        01-0CT-2002 (TrEMBLE) 22,
01-0CT-2002 (TrEMBLE) 22,
01-MAR-2003 (TrEMBLE) 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cuery Match
Best Local Similarity 88.3%
Matches 242; Conservative
                                                                                                                                                                                                                                              PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                             SEÇUSNOE FROM N.A.
D'Agara V
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                      Parkin isoform
                                                                                                                                                                                                                                              08NI44
                                                                                                                                                                                                                   RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 QCNHPHVICEDCFBLYCVTRENDRQFVHDAQLGYSLPCVAGCPNSLIKELEHFRILGERG 310
                                                                                                                                                                                       SCWDDVLIPNRMSGECQSPDCPGTRAEFFFKCGAHPTSDKDTSVALNLITSNRRSIPCTA 239
                                                                                                                                                                                                        301 ALGGFRRGVAGCPNSLIKELHHPRILGEBQYNRYQQYGARECVLQMGGVICPR9GGAGL 369
                                                                      61 LEQOSIVHIVGRPRRSHETNASGGDEPGSINESRSLIRVDLSSHTUPVDSVGLA 120
                                                                                                                             121 VILDTDSKROSERARGPV-KPTYNSFFIYCKGPCHKVQPGKLRVQCGTCKQATLTLAQGP 179
                                                                                                                                                                                                                                                                                                       289 ------VAGCPNSLIKELHHFRILGESQYTRYQQYGABECVLQMGGVLCPRPGCGAGL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                 61 LOQQSIVHIVQRPWRKGQEMNATGGDERRAAGGCEREPQSLARVOLSSSVLPGOSVGLA
                                                                                                                                               240 CTDVRSPVLVFQCNHRHVICLDCFHLYCVTRLNDRQFVHDAQLGYSUFC-------
               MIVEVRENSSYGFPVEVDSDTSILOLKEVVAKROGVPADQLRVIFAGKELPNHLTVQNCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cuery Match 59.6%; Score 1512; CB 11; Length 274; Best Local Similarity 96.4%; Pred. No. 4.2e-136; Matches 264; Conservative 6; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D'Agata V.M., Scapagnini G., Cavallaro S.;
"Functional and molecular diversity of parkin in the rat
Submitted (JAN-2001) to the EMBL/GenBank/DDB3 databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D'Agata V., Scapagnini G., Cavallaro S.,
"Functional and molecular diversity of parkin.";
"Functional and molecular diversity of parkin.";
Submitted (MAY-2001) to the EXBL/GenBank/DDBJ databases.
EMBL; AF391280; AAM21455.1;
InterPro; IPR00169; SHpror_acsite.
InterPro; IPR002867; parkin.
InterPro; IPR002867; Znf_C6HC.
Pfam; PF01485; IBR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01475; PARKIN.
PROSITE; PS0119; THIOL PROTEASE CYS; 1.
SEQUENCE 274 AA; 30642 MM; BZ9BBS8E86EB5DFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBirel. 20, Created)
01-MAR-2002 (TrEMBirel. 20, Last sequence update)
01-MAR-2003 (TrEMBirel. 23, Last annotation update)
Parkin transcript variant 6 (Parkin isoform).
Rattus norvegious (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                  361 LPEPDQRKVTCEGGNGLGCGY 381
                                                                                                                                                                                                                                                                                                                                                                341 LPEQGQRKVTCEGGNGLGCGF 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                       180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CCNSRHVICLDCPHLYCVTRLNDRQPVHOPQLGYSLPCVAGCPNSLIKELHHFRILGEEQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YHEGDCDSLLEPSGATSQAYRVDKRAAEQARWEEASKETIKKTTKPCPRCNVPIFKNGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Hono sapiens (Human).
Bukaryota, Metazoa, Chordana, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutberia, Primanes, Catarrini, Hominidac, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Indeis
                                                                                                                                  P. Agata V., Scappgnini G., Cavallaro S., Functional and molecular diversity of parkin."; Submitted MAY-2001 to the EMBL/GenBank/DCBC databases. EMBL) AF38-282: AAX21457.1; -10.ExPro.; PR003977; parkin. InterPro.; IPR003977; parkin. InterPro.; IPR00269; SHproc. Acsine. InterPro.; IPR02069; CMC GHC. Pfan; PPC1455; IBR.; 2. PRINTS; PR01475; PARKIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel, 16, Created)
(TrEMBLrel, 16, Last sequence update)
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096522
10 096522
AC 095522:
DT 01 WAR-2001 (7
DT 01 WAR-2001 (7
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61 LEQOSIVHINGRPRERSHETHASGGDEPQSTSEGSIMESRSLTRVDLSSHTLPVDSNGLA 120
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Stapleton M., Brokstein F., Hong i., Agbayani A., Carlson J.,

Stapleton M., Brokstein F., Hong i., Agbayani A., Carlson J.,

R. Charbe M., Chavez C., Dorsett V., Farfan D., Frise E.,

Ronzalez M., Guarin H., ii. F. F.

R. Charbe M., Carleb J., Paragas V., Park S., Phouaneravong E., Wan K.,

R. Minoo J., Pacaleb J., Paragas V., Park S., Phouaneravong E., Wan K.,

R. Demit C. Lewis S.E., Rubin G.M., Celniker S.,

Rubinted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

Bubmitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

Rubinted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

Bubmitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

Bubmitted (OCT-2001) parkin.

Britant Projour JPRO2066; Ubquitin.

Britant Projour JPRO2066; Ubquitin.

Britant Projour JPRO2066; Ubquitin.

Britant Projour JPRO3066; Ubquitin.

Britant JPRO3068; Ub
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MIVEVRENSSYGEPVSVDSOTSILQLKSVVAKRQSVPADQLRVIFAGKELPNHLTVQNCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIVEVRENSSYGEPVEVOSDISILOLKEVVAKROGVPADQURVIFAGKELPHELIVONOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LEQQSIVHIVQRPRRRSHETWASSGDEPQSTSBGSIWESRSLTRVDLSSHTLFVDSVGLA
                                                                                                                                                                                                                                                                                                                      DB 11; Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Haxapoda, Insecta, Pterygota,
Meptera, Edopterygota, Diplera, Brachycera, Muscomorpha,
Mepterodoa, Drosophilidae, Brosophila.
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.6%; Pred. No. 4.26-112;
Matches 243; Conservative 0; Mismatches 0; Indels
MGD, MGI:1355286, Park2.
InterPro, IPR003977, parkin.
InterPro, IPR00526, Ub-quinin.
PFGM, PF004040, PARKIN.
PFRINTS, PR01475, PARKIN.
PRINTS, PR01475, UBCUININ.
SMAPT, SW00213, UBCUININ.
SMAPT, SW00213, UBQUITIN.
SEQUENCE. 262 Aa; 28700 MW; CDCE80F2956551AE CR064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update;
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              482 AA
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01-DEC-2001 (TEMBERE), 19, Created;
01-DEC-2001 (TEMBERE) 19, Last seq
01-MAR-2003 (TEMBERE) 23, Last ann
5509-479F;
PARKIK CR CG10523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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24: CTDV 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                             Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Suteleostomi;
Mammalla; Sutheria; Rodentia; Schurognathi; Muridae; Murinae; Mus
NCSI TAXID=10096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Bukaryota; Merazoa: Chordata; Craniata; Verrebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=BALB/C: TISSID=Brain;
STSTAIN=BALB/C: TISSID=Brain;
Stichel C.C., Augustin M., Kuhn K., Zhu X., Engels P., Ulmer C.,
Lubbert H.;
"Parkin expression in the adult mouse brain.";
Submitred (MAR-2000) to the EMBL/GenBank/DDBJ databases.
BMBJ: AF250249; AAG13891.1; -.
HSSP; P02248; 1UBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAINSHALB/C; IISSUE=Kidney;
Stribel C.C., Augustin M., Kuhn K., Zhu X., Engels P., Ulmer (Lubbert H.;
"Parkin expression in the adult mouse brain.";
Submitted (MAR-2000; to the EXBL/GenBank/DD3J databases.
ENBL; AF252295; AAG13892.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

Best Local Similarity 99.6%; Pred. No. 1.6e-112;
Matches 244; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SX00213; UBQ; 1.
PROSITE; PS50053; UBIQUITIN 2; 1.
SEQUENCE 25S AA; 28155 NW; D2EEC07EC954C11A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
      01-MAR-2003 (Trembirel, 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1355296; Park2.
InterPro; IPR003977; parkin.
InterPro; IPR000626; Ubiquicin.
Pro; Pro0340; ubiquicin; 1.
PRINTS; PR01475; PARKIN.
PRINTS; PR00348; UBIQUITIN.
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01-MAR-2001 (TYEMBLE) 16,
01-MAR-2003 (TYEMBLE) 23,
                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 | | | CTOVR 245
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PARK2.
                                       Parkin
                                                                     PARK2
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COES23
COES2
AC 09522
AC 09522
DT 01-MA
DT 01-M
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Madams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

B. Sutton G.G., Wortman J.R., Richards S.A., Ashburner M., Hefiffer B.D.,

Aman K.H., Doyle C., Bazer E.G., Helt G., Kalson C.R., Miklos G.L.G.,

Abril J.F., Apdayari A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,

Ballew R.M., Basu A., Baxendale J., Bayraktarogiu L., Beasley E.N.,

Ballew R.M., Basu A., Baxendale J., Bayraktarogiu L., Beasley E.N.,

Beron K.Y., Benos P.W., Berman B.P., Biandari D., Bottier P.,

Borkova D., Botchan M.R., Butler H., Cadzeu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Danke C., Davenport L.B., Davies P.,

Cherry J.M., Cawley S., Danke C., Ferraz C., Ferriera S., Fleischmann M.,

Codson K., Doup L.E., Downes M., Dugan-Rocha S., Junkov B.C.,

Coloris C., Gabrielian A.E., Garg N.S., Gelbart M., Glodek A., Gong F., Gorell J.H., Qu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck C.,
                                                     12;
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                                                                                                  3 VEVRENSSYGFPVEVDSDISILQLKEVVAKRQGVPADQLRVIFAGKELPNHLTVQNCDLE
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
       Length 482;
                                                     Indels
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Last sequence update)
Last annotation update)
Query Match
41.9%; Score 1078; DB 5;
Best Local Similarity 43.7%; Pred. No. 5.3e-93;
Matches 209; Conservative 78; Mismatches 145;
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InterPro; IPR003977; parkin.
InterPro; IPR000626; Ubiquitin.
InterPro; IPR002667; Znf_C6HC.
Pfam; PF00245; Ubiquitin; 1.
Pfam; PF00245; ubiquitin; 1.
PRINTS; PR01475; PAKIN.
PRINTS; PR01475; PAKIN.
SMART; SM00213; UBQ; 1.
PR031TE; PS00092; NE MINSE; 1.
PROSITE; PS00093; NE MINSE; 1.
PROSITE; PS00093; NE MINSE; 1.
PROSITE; PS00093; UBIQUITIN 2; 1.
SEQUENCE 492 AA; 54104 MW; 4A89C695475E213D CRC64;
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